

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3288	cyclops	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/08/17 17:01
L2	8	L1 and retro\$1element	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/08/17 17:02
S1	7	"6331662"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/08/17 17:01
S2	5	"6720479"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/08/01 15:19
S3	2	"6949695"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/08/01 15:19

=> d his

(FILE 'HOME' ENTERED AT 17:04:48 ON 17 AUG 2006)

FILE 'AGRICOLA, CABA, CAPLUS, BIOSIS' ENTERED AT 17:04:55 ON 17 AUG 2006

L1	6666 S ((WRIGHT D?) OR (WRIGHT, D?))/AU
L2	0 S L1 AND TRANSPOSON
L3	13 S L1 AND RETROELEMENT
L4	9 DUP REM L3 (4 DUPLICATES REMOVED)
L5	159 S ((VOYTAS D?) OR (VOYTAS, D?))/AU
L6	41 S L5 AND RETROELEMENT
L7	22 DUP REM L6 (19 DUPLICATES REMOVED)
L8	1755 S RETROELEMENT
L9	728 S L8 AND PLANT
L10	5 S L9 AND CYCLOPS
L11	2 DUP REM L10 (3 DUPLICATES REMOVED)
L12	5 S L10 AND GYPSY
L13	2 DUP REM L12 (3 DUPLICATES REMOVED)
L14	50 S PRIMER BINDING SITE AND RETROELEMENT
L15	24 DUP REM L14 (26 DUPLICATES REMOVED)
L16	11 S L15 AND PLANT

SCORE Search Results Details for Application 10 and Search Result us-10-615-005-1.rng.

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This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:55:39 ; Search time 344.25 Seconds
(without alignments)
364.562 Million cell updates/sec

Title: US-10-615-005-1
Perfect score: 18
Sequence: 1 tggcgccggttgccaattg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	18	100.0	18	3	AAZ35269	Aaz35269 Plant ret
2	18	100.0	28	10	ADJ81544	Adj81544 Plant ret
3	18	100.0	28	10	ADJ81545	Adj81545 Plant ret
4	18	100.0	28	10	ADJ81547	Adj81547 Plant ret
5	18	100.0	149	3	AAZ35270	Aaz35270 Plant ret
6	18	100.0	13868	10	ADJ81501	Adj81501 Plant ret
7	18	100.0	13894	10	ADJ81499	Adj81499 Plant ret
8	18	100.0	13938	10	ADJ81503	Adj81503 Plant ret
9	18	100.0	13966	10	ADJ81500	Adj81500 Plant ret
10	18	100.0	14005	10	ADJ81504	Adj81504 Plant ret
11	18	100.0	14016	10	ADJ81505	Adj81505 Plant ret
c 12	18	100.0	59590	3	AAF22281	Aaf22281 BAC conta
c 13	18	100.0	64415	3	AAF22279	Aaf22279 BAC conta
14	18	100.0	82138	3	AAF22305_10	Continuation (11 o
c 15	18	100.0	83390	3	AAF22283	Aaf22283 BAC conta
c 16	18	100.0	90336	3	AAF22289	Aaf22289 BAC conta
c 17	18	100.0	92584	3	AAF22288	Aaf22288 BAC conta
c 18	18	100.0	94895	3	AAF22302	Aaf22302 BAC conta
c 19	18	100.0	95223	3	AAF22282	Aaf22282 BAC conta
c 20	18	100.0	96583	3	AAF22297	Aaf22297 BAC conta
21	18	100.0	96988	3	AAF22290	Aaf22290 BAC conta
22	18	100.0	109973	3	AAF22298	Aaf22298 BAC conta
c 23	18	100.0	110000	3	AAF22303_0	Aaf22303 Arabidops
24	18	100.0	134499	3	AAF22286	Aaf22286 BAC conta
c 25	17	94.4	40349	3	AAF22278	Aaf22278 BAC conta
26	17	94.4	86584	3	AAF22292	Aaf22292 BAC conta
c 27	17	94.4	151826	3	AAF22291	Aaf22291 BAC conta
28	16.4	91.1	13320	10	ADJ81502	Adj81502 Plant ret
c 29	16.4	91.1	50959	3	AAF22304	Aaf22304 Arabidops
30	16.4	91.1	64415	3	AAF22279	Aaf22279 BAC conta
c 31	16.4	91.1	72592	3	AAF22300	Aaf22300 BAC conta
32	16.4	91.1	79122	3	AAF22294	Aaf22294 BAC conta
33	16.4	91.1	83390	3	AAF22283	Aaf22283 BAC conta
c 34	16.4	91.1	86584	3	AAF22292	Aaf22292 BAC conta
35	16.4	91.1	90336	3	AAF22289	Aaf22289 BAC conta
c 36	16.4	91.1	103929	3	AAF22287	Aaf22287 BAC conta
37	16.4	91.1	110000	3	AAF22305_08	Continuation (9 of
38	16.4	91.1	110000	3	AAF22305_09	Continuation (10 o
c 39	16.4	91.1	134499	3	AAF22286	Aaf22286 BAC conta
c 40	15.4	85.6	416	13	ACN61720	Acn61720 Cotton gy
c 41	15.4	85.6	548	3	AAA82386	Aaa82386 N. mening
c 42	15.4	85.6	1395	8	ACA30133	Aca30133 Prokaryot
c 43	15.4	85.6	1713	2	AAT36389	Aat36389 Aryl Beta
c 44	15.4	85.6	1713	3	AAZ38242	Aaz38242 Vibrio fu
c 45	15.4	85.6	8778	4	ABL29794	Abl29794 Drosophil
46	15.4	85.6	80450	3	AAF22295	Aaf22295 BAC conta
c 47	15.4	85.6	82138	3	AAF22305_10	Continuation (11 o
48	15.4	85.6	82588	3	AAF22301	Aaf22301 BAC conta
49	15.4	85.6	94895	3	AAF22302	Aaf22302 BAC conta
50	15.4	85.6	110000	3	AAF22305_00	Aaf22305 Arabidops
c 51	15.4	85.6	110000	3	AAF22305_09	Continuation (10 o
c 52	15.4	85.6	110000	14	AEB39175_26	Continuation (27 o
c 53	15.4	85.6	110000	14	AEB39175_27	Continuation (28 o
54	15.4	85.6	163319	3	AAF22306	Aaf22306 Arabidops
55	15.4	85.6	189430	14	AEB35718	Aeb35718 L. pneumo
c 56	15	83.3	412	3	AAA79678	Aaa79678 Pinus rad

<http://es.ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549954&ItemName=...> 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	18	100.0	18	2	AR264375	AR264375 Sequence
2	18	100.0	18	2	AR494850	AR494850 Sequence
3	18	100.0	18	2	AR779190	AR779190 Sequence
4	18	100.0	150	2	AR264401	AR264401 Sequence
5	18	100.0	150	2	AR494876	AR494876 Sequence
6	18	100.0	150	2	AR779216	AR779216 Sequence
c 7	18	100.0	3539	4	AB073161	AB073161 Arabidops
8	18	100.0	18433	4	AC093090	AC093090 Arabidops
c 9	18	100.0	18813	4	T9E19	AF104920 Arabidops
10	18	100.0	32259	12	AC109921	AC109921 Arabidops
11	18	100.0	33329	4	AC007261	AC007261 Arabidops
c 12	18	100.0	35551	2	AX059461	AX059461 Sequence
13	18	100.0	36032	2	AX059500	AX059500 Sequence
14	18	100.0	38519	2	AX059548	AX059548 Sequence
15	18	100.0	39104	2	AX059479	AX059479 Sequence
c 16	18	100.0	40480	2	AX059456	AX059456 Sequence
c 17	18	100.0	42112	2	AX059497	AX059497 Sequence
c 18	18	100.0	42208	2	AX059477	AX059477 Sequence
c 19	18	100.0	47383	2	AX059459	AX059459 Sequence
c 20	18	100.0	47840	2	AX059452	AX059452 Sequence
21	18	100.0	48128	2	AX059469	AX059469 Sequence
c 22	18	100.0	48128	2	AX059474	AX059474 Sequence
c 23	18	100.0	48128	2	AX059513	AX059513 Sequence
c 24	18	100.0	48422	2	AX059509	AX059509 Sequence
25	18	100.0	50349	4	AC079028	AC079028 Arabidops
c 26	18	100.0	52015	4	AB086244	AB086244 Arabidops
27	18	100.0	52616	12	AC090029	AC090029 Arabidops
c 28	18	100.0	54573	4	T6L9	AF147265 Arabidops
c 29	18	100.0	55345	4	AC007209	AC007209 Arabidops
30	18	100.0	57000	4	AB046428	AB046428 Arabidops
c 31	18	100.0	57000	4	AB046428	AB046428 Arabidops
32	18	100.0	58411	4	AB046430	AB046430 Arabidops
c 33	18	100.0	58411	4	AB046430	AB046430 Arabidops
c 34	18	100.0	59590	2	AR777032	AR777032 Sequence
35	18	100.0	60482	12	AC090030	AC090030 Arabidops
36	18	100.0	62916	4	AB046427	AB046427 Arabidops
37	18	100.0	64165	4	AC067965	AC067965 Genomic s
c 38	18	100.0	64415	2	AR777030	AR777030 Sequence
39	18	100.0	65316	4	F14C23	AF296828 Arabidops
40	18	100.0	66542	4	T10I18	AF262040 Arabidops
c 41	18	100.0	68352	4	T15F17	AF262042 Arabidops
c 42	18	100.0	69752	4	T5H22	AF096372 Arabidops
c 43	18	100.0	74265	4	AC068901	AC068901 Arabidops
44	18	100.0	76911	12	AC016828	AC016828 Arabidops
c 45	18	100.0	77287	4	AB026642	AB026642 Arabidops
46	18	100.0	80279	12	AC011624	AC011624 Arabidops
c 47	18	100.0	81414	4	AB024037	AB024037 Arabidops
c 48	18	100.0	81806	4	AB062087	AB062087 Arabidops
49	18	100.0	81902	4	T17A2	AF160183 Arabidops
c 50	18	100.0	81902	4	T17A2	AF160183 Arabidops
51	18	100.0	82144	2	AR777056_10	Continuation (11 o
c 52	18	100.0	83129	12	AC009529	AC009529 Arabidops

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-1.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 09:07:39 ; Search time 116.25 Seconds
(without alignments)
289.720 Million cell updates/sec

Title: US-10-615-005-1
Perfect score: 18
Sequence: 1 tggcgccgttgccaattg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	IDB	Description
------------	-------	--------------------	-----	-------------

1	18	100.0	18	3	US-09-322-478-1	Sequence 1, Appli
2	18	100.0	18	3	US-09-586-106D-1	Sequence 1, Appli
3	18	100.0	18	3	US-10-799-870-1	Sequence 1, Appli
4	18	100.0	150	3	US-09-322-478-36	Sequence 36, Appl
5	18	100.0	150	3	US-09-586-106D-36	Sequence 36, Appl
6	18	100.0	150	3	US-10-799-870-36	Sequence 36, Appl
c 7	18	100.0	59590	4	US-09-531-120-187	Sequence 187, App
c 8	18	100.0	64415	4	US-09-531-120-185	Sequence 185, App
c 9	18	100.0	83391	4	US-09-531-120-189	Sequence 189, App
c 10	18	100.0	90336	4	US-09-531-120-195	Sequence 195, App
c 11	18	100.0	92584	4	US-09-531-120-194	Sequence 194, App
c 12	18	100.0	94905	4	US-09-531-120-208	Sequence 208, App
c 13	18	100.0	95223	4	US-09-531-120-188	Sequence 188, App
c 14	18	100.0	96583	4	US-09-531-120-203	Sequence 203, App
15	18	100.0	96988	4	US-09-531-120-196	Sequence 196, App
16	18	100.0	109974	4	US-09-531-120-204	Sequence 204, App
17	18	100.0	134499	4	US-09-531-120-192	Sequence 192, App
c 18	18	100.0	611587	4	US-09-531-120-209	Sequence 209, App
19	18	100.0	1082144	4	US-09-531-120-211	Sequence 211, App
c 20	17	94.4	40349	4	US-09-531-120-184	Sequence 184, App
21	17	94.4	86585	4	US-09-531-120-198	Sequence 198, App
c 22	17	94.4	151828	4	US-09-531-120-197	Sequence 197, App
c 23	16.4	91.1	50959	4	US-09-531-120-210	Sequence 210, App
24	16.4	91.1	64415	4	US-09-531-120-185	Sequence 185, App
c 25	16.4	91.1	72600	4	US-09-531-120-206	Sequence 206, App
26	16.4	91.1	79122	4	US-09-531-120-200	Sequence 200, App
27	16.4	91.1	83391	4	US-09-531-120-189	Sequence 189, App
c 28	16.4	91.1	86585	4	US-09-531-120-198	Sequence 198, App
29	16.4	91.1	90336	4	US-09-531-120-195	Sequence 195, App
c 30	16.4	91.1	103931	4	US-09-531-120-193	Sequence 193, App
c 31	16.4	91.1	134499	4	US-09-531-120-192	Sequence 192, App
c 32	15.4	85.6	1713	2	US-08-386-727-5	Sequence 5, Appli
c 33	15.4	85.6	1713	2	US-08-600-452A-5	Sequence 5, Appli
34	15.4	85.6	80450	4	US-09-531-120-201	Sequence 201, App
35	15.4	85.6	82596	4	US-09-531-120-207	Sequence 207, App
36	15.4	85.6	94905	4	US-09-531-120-208	Sequence 208, App
37	15.4	85.6	163317	4	US-09-531-120-212	Sequence 212, App
c 38	15.4	85.6	1082144	4	US-09-531-120-211	Sequence 211, App
c 39	15	83.3	412	3	US-10-101-464A-479	Sequence 479, App
c 40	15	83.3	163317	4	US-09-531-120-212	Sequence 212, App
41	14.8	82.2	570	3	US-09-252-991A-10538	Sequence 10538, A
42	14.8	82.2	573	5	US-09-974-300-4705	Sequence 4705, Ap
c 43	14.8	82.2	984	3	US-09-252-991A-10329	Sequence 10329, A
44	14.8	82.2	987	3	US-09-489-039A-2135	Sequence 2135, Ap
c 45	14.8	82.2	1089	5	US-09-974-300-764	Sequence 764, App
46	14.8	82.2	1272	3	US-09-053-702-1	Sequence 1, Appli
47	14.8	82.2	1299	3	US-09-543-681A-3729	Sequence 3729, Ap
48	14.8	82.2	1425	3	US-09-540-236-972	Sequence 972, App
c 49	14.8	82.2	1869	3	US-09-543-681A-3350	Sequence 3350, Ap
c 50	14.8	82.2	3097	3	US-09-282-147-38	Sequence 38, Appl
c 51	14.8	82.2	3097	3	US-10-216-981A-2	Sequence 2, Appli
52	14.8	82.2	101786	4	US-09-531-120-199	Sequence 199, App
53	14.8	82.2	129021	4	US-09-531-120-202	Sequence 202, App
c 54	14.8	82.2	269223	3	US-09-596-002-41	Sequence 41, Appl
c 55	14.4	80.0	189	3	US-09-252-991A-15695	Sequence 15695, A
56	14.4	80.0	750	3	US-09-252-991A-15662	Sequence 15662, A
c 57	14.4	80.0	962	3	US-09-072-596-310	Sequence 310, App
c 58	14.4	80.0	962	3	US-09-072-967-315	Sequence 315, App
c 59	14.4	80.0	962	3	US-10-193-002-310	Sequence 310, App
c 60	14.4	80.0	962	3	US-10-084-843-315	Sequence 315, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	3	US-09-965-553-1	Sequence 1, Appli
	2	18	100.0	18	8	US-10-615-005-1	Sequence 1, Appli
	3	18	100.0	18	8	US-10-395-607-1	Sequence 1, Appli
	4	18	100.0	18	8	US-10-799-870-1	Sequence 1, Appli
	5	18	100.0	30	7	US-10-315-515-2	Sequence 2, Appli
	6	18	100.0	30	7	US-10-315-515-3	Sequence 3, Appli
	7	18	100.0	30	7	US-10-315-515-5	Sequence 5, Appli
	8	18	100.0	150	3	US-09-965-553-36	Sequence 36, Appl
	9	18	100.0	150	8	US-10-615-005-36	Sequence 36, Appl
	10	18	100.0	150	8	US-10-395-607-36	Sequence 36, Appl
	11	18	100.0	150	8	US-10-799-870-36	Sequence 36, Appl
	12	18	100.0	13868	7	US-10-315-515-123	Sequence 123, App
	13	18	100.0	13894	7	US-10-315-515-121	Sequence 121, App
	14	18	100.0	13938	7	US-10-315-515-125	Sequence 125, App
	15	18	100.0	13966	7	US-10-315-515-122	Sequence 122, App
	16	18	100.0	14005	7	US-10-315-515-126	Sequence 126, App
	17	18	100.0	14016	7	US-10-315-515-127	Sequence 127, App
c	18	18	100.0	59590	15	US-11-117-187-187	Sequence 187, App
c	19	18	100.0	64415	15	US-11-117-187-185	Sequence 185, App
c	20	18	100.0	83391	15	US-11-117-187-189	Sequence 189, App
c	21	18	100.0	90336	15	US-11-117-187-195	Sequence 195, App
c	22	18	100.0	92584	15	US-11-117-187-194	Sequence 194, App
c	23	18	100.0	94905	15	US-11-117-187-208	Sequence 208, App
c	24	18	100.0	95223	15	US-11-117-187-188	Sequence 188, App
c	25	18	100.0	96583	15	US-11-117-187-203	Sequence 203, App
	26	18	100.0	96988	15	US-11-117-187-196	Sequence 196, App
	27	18	100.0	109974	15	US-11-117-187-204	Sequence 204, App
	28	18	100.0	134499	15	US-11-117-187-192	Sequence 192, App
c	29	18	100.0	611587	15	US-11-117-187-209	Sequence 209, App
	30	18	100.0	1082144	15	US-11-117-187-211	Sequence 211, App
c	31	17	94.4	40349	15	US-11-117-187-184	Sequence 184, App
	32	17	94.4	86585	15	US-11-117-187-198	Sequence 198, App
c	33	17	94.4	151828	15	US-11-117-187-197	Sequence 197, App
	34	16.4	91.1	13320	7	US-10-315-515-124	Sequence 124, App
c	35	16.4	91.1	50959	15	US-11-117-187-210	Sequence 210, App
	36	16.4	91.1	64415	15	US-11-117-187-185	Sequence 185, App
c	37	16.4	91.1	72600	15	US-11-117-187-206	Sequence 206, App
	38	16.4	91.1	79122	15	US-11-117-187-200	Sequence 200, App
	39	16.4	91.1	83391	15	US-11-117-187-189	Sequence 189, App
c	40	16.4	91.1	86585	15	US-11-117-187-198	Sequence 198, App
	41	16.4	91.1	90336	15	US-11-117-187-195	Sequence 195, App
c	42	16.4	91.1	103931	15	US-11-117-187-193	Sequence 193, App
c	43	16.4	91.1	134499	15	US-11-117-187-192	Sequence 192, App
c	44	15.4	85.6	416	8	US-10-021-323-16501	Sequence 16501, A
c	45	15.4	85.6	548	10	US-10-915-740A-933	Sequence 933, App
c	46	15.4	85.6	556	4	US-09-925-065A-427081	Sequence 427081,
c	47	15.4	85.6	556	5	US-09-925-065A-427081	Sequence 427081,
c	48	15.4	85.6	1363	8	US-10-437-963-53305	Sequence 53305, A
c	49	15.4	85.6	1395	8	US-10-282-122A-18003	Sequence 18003, A
c	50	15.4	85.6	8778	13	US-11-097-143-41932	Sequence 41932, A
	51	15.4	85.6	80450	15	US-11-117-187-201	Sequence 201, App

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-1.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-1.rnpbn.

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OM nucleic - nucleic search, using sw model

```
Run on:      June 29, 2006, 09:33:22 ; Search time 818.25 Seconds
              (without alignments)
              26.013 Million cell updates/sec
```

Title: US-10-615-005-1
Perfect score: 18
Sequence: 1 tggcgccggttgccaattg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_NA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query
--------	-------

No.	Score	Match	Length	DB	ID	Description
c 1	15.4	85.6	1080	7	US-11-266-748A-232039	Sequence 232039,
c 2	14.8	82.2	204	7	US-11-217-529-173148	Sequence 173148,
3	14.8	82.2	390	7	US-11-217-529-82190	Sequence 82190, A
c 4	14.8	82.2	453	7	US-11-217-529-77223	Sequence 77223, A
c 5	14.8	82.2	537	7	US-11-217-529-82169	Sequence 82169, A
6	14.8	82.2	601	6	US-10-449-902-10348	Sequence 10348, A
7	14.8	82.2	888	7	US-11-217-529-80215	Sequence 80215, A
8	14.8	82.2	1242	6	US-10-449-902-324	Sequence 324, App
9	14.8	82.2	1257	6	US-10-449-902-126	Sequence 126, App
10	14.8	82.2	1298	6	US-10-449-902-22329	Sequence 22329, A
11	14.8	82.2	1451	6	US-10-449-902-8176	Sequence 8176, Ap
12	14.8	82.2	1653	7	US-11-217-529-173346	Sequence 173346,
c 13	14.8	82.2	1902	6	US-10-449-902-22996	Sequence 22996, A
c 14	14.8	82.2	1951	6	US-10-449-902-11988	Sequence 11988, A
c 15	14.8	82.2	3537	7	US-11-266-748A-30301	Sequence 30301, A
16	14.4	80.0	942	6	US-10-471-571A-4457	Sequence 4457, Ap
c 17	14.4	80.0	1312	6	US-10-449-902-12575	Sequence 12575, A
18	14.4	80.0	1457	6	US-10-449-902-27525	Sequence 27525, A
19	14.4	80.0	2661	6	US-10-449-902-16156	Sequence 16156, A
c 20	14	77.8	1060	6	US-10-953-349-28878	Sequence 28878, A
c 21	14	77.8	1491	7	US-11-189-375A-16	Sequence 16, Appl
22	14	77.8	1698	7	US-11-216-545-7930	Sequence 7930, Ap
c 23	14	77.8	2937	6	US-10-449-902-27503	Sequence 27503, A
24	13.8	76.7	25	7	US-11-217-529-181721	Sequence 181721,
25	13.8	76.7	297	7	US-11-217-529-173775	Sequence 173775,
c 26	13.8	76.7	707	6	US-10-449-902-16263	Sequence 16263, A
c 27	13.8	76.7	735	7	US-11-266-748A-44563	Sequence 44563, A
28	13.8	76.7	775	7	US-11-266-748A-208956	Sequence 208956,
c 29	13.8	76.7	833	7	US-11-266-748A-79989	Sequence 79989, A
30	13.8	76.7	833	7	US-11-266-748A-132800	Sequence 132800,
c 31	13.8	76.7	890	7	US-11-266-748A-26228	Sequence 26228, A
c 32	13.8	76.7	890	7	US-11-266-748A-31480	Sequence 31480, A
c 33	13.8	76.7	890	7	US-11-266-748A-224417	Sequence 224417,
c 34	13.8	76.7	890	7	US-11-266-748A-405361	Sequence 405361,
35	13.8	76.7	890	7	US-11-266-748A-476407	Sequence 476407,
36	13.8	76.7	1000	7	US-11-266-748A-408704	Sequence 408704,
c 37	13.8	76.7	1000	7	US-11-266-748A-479750	Sequence 479750,
c 38	13.8	76.7	1007	7	US-11-266-748A-362621	Sequence 362621,
39	13.8	76.7	1007	7	US-11-266-748A-446000	Sequence 446000,
c 40	13.8	76.7	1295	6	US-10-449-902-3306	Sequence 3306, Ap
c 41	13.8	76.7	1323	6	US-10-449-902-3799	Sequence 3799, Ap
c 42	13.8	76.7	1323	6	US-10-449-902-4128	Sequence 4128, Ap
c 43	13.8	76.7	1380	6	US-10-953-349-32604	Sequence 32604, A
c 44	13.8	76.7	1506	6	US-10-449-902-15356	Sequence 15356, A
45	13.8	76.7	1738	6	US-10-449-902-17914	Sequence 17914, A
c 46	13.8	76.7	1770	7	US-11-266-748A-185429	Sequence 185429,
47	13.8	76.7	1800	7	US-11-217-529-78845	Sequence 78845, A
c 48	13.8	76.7	2199	7	US-11-266-748A-185430	Sequence 185430,
c 49	13.8	76.7	2199	7	US-11-266-748A-192922	Sequence 192922,
50	13.8	76.7	2409	6	US-10-449-902-22638	Sequence 22638, A
51	13.8	76.7	2512	6	US-10-449-902-19615	Sequence 19615, A
52	13.8	76.7	2682	7	US-11-121-154-70	Sequence 70, Appl
c 53	13.8	76.7	2728	6	US-10-449-902-12964	Sequence 12964, A
c 54	13.8	76.7	2940	7	US-11-217-529-77568	Sequence 77568, A
c 55	13.8	76.7	3046	6	US-10-449-902-18291	Sequence 18291, A
c 56	13.8	76.7	3179	7	US-11-266-748A-356269	Sequence 356269,
c 57	13.8	76.7	3179	7	US-11-266-748A-385811	Sequence 385811,
58	13.8	76.7	3179	7	US-11-266-748A-439648	Sequence 439648,
c 59	13.8	76.7	404123	7	US-11-266-748A-23884	Sequence 23884, A

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-1.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-1.rst.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 09:05:40 ; Search time 2757.75 Seconds
(without alignments)
364.989 Million cell updates/sec

Title: US-10-615-005-1
Perfect score: 18
Sequence: 1 tggcgccggttgccaattg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	18	100.0	129	3	BQ853899	BQ853899 QGB21M16.
	2	18	100.0	166	14	AL771403	AL771403 Arabidops
c	3	18	100.0	177	14	AL757122	AL757122 Arabidops
	4	18	100.0	178	11	AQ958189	AQ958189 LERAV83TF
	5	18	100.0	193	14	CR933908	CR933908 Arabidops
	6	18	100.0	199	11	BH243164	BH243164 AUIHC32TR
c	7	18	100.0	216	14	CNS00T11	AL089107 Arabidops
	8	18	100.0	232	14	CR405092	CR405092 Arabidops
	9	18	100.0	239	14	CR405093	CR405093 Arabidops
	10	18	100.0	263	11	BH243803	BH243803 AUIRB17TR
	11	18	100.0	268	14	CR933907	CR933907 Arabidops
	12	18	100.0	273	14	AL946614	AL946614 Arabidops
c	13	18	100.0	388	11	B62585	B62585 T22F21TF TA
	14	18	100.0	401	11	BH244138	BH244138 AUIWA26TF
c	15	18	100.0	410	11	BH244101	BH244101 AUIWA38TR
	16	18	100.0	415	11	BH243289	BH243289 AUIHF63TR
c	17	18	100.0	418	11	BH243156	BH243156 AUIHC93TR
	18	18	100.0	419	11	BH252783	BH252783 SALK_0138
c	19	18	100.0	422	11	BH244105	BH244105 AUIWA21TR
	20	18	100.0	424	11	BH244079	BH244079 AUIRB53TR
	21	18	100.0	437	11	BH244067	BH244067 AUIRF34TR
	22	18	100.0	439	11	BH243367	BH243367 AUIRF77TR
c	23	18	100.0	444	11	BH243576	BH243576 AUIRC53TR
	24	18	100.0	446	11	BH235368	BH235368 AUIVA26TR
	25	18	100.0	451	14	CNS00MQ7	AL080941 Arabidops
	26	18	100.0	452	14	CNS00O1V	AL082657 Arabidops
	27	18	100.0	455	14	CNS00R39	AL086595 Arabidops
	28	18	100.0	456	3	BQ989005	BQ989005 QGF16H19.
c	29	18	100.0	457	11	AQ958592	AQ958592 LERAY51TR
	30	18	100.0	460	11	B95970	B95970 F21D2TFC IG
	31	18	100.0	470	11	BH235524	BH235524 AUIVC40TF
	32	18	100.0	471	14	CNS00MSM	AL081028 Arabidops
	33	18	100.0	478	11	BH243935	BH243935 AUIRA20TF
	34	18	100.0	483	14	CNS00MGM	AL080596 Arabidops
	35	18	100.0	486	11	B23757	B23757 F16P22TR IG
	36	18	100.0	493	11	BH243182	BH243182 AUIHD82TF
c	37	18	100.0	493	11	BH243582	BH243582 AUIRE65TF
	38	18	100.0	493	11	BH243774	BH243774 AUIRF06TF
	39	18	100.0	495	10	DW174610	DW174610 CLVZ5568.
	40	18	100.0	502	10	DW174654	DW174654 CLVZ5608.
	41	18	100.0	505	14	CNS00OVV	AL083737 Arabidops
	42	18	100.0	506	11	B27265	B27265 T3D23TF TAM
c	43	18	100.0	514	11	BH243704	BH243704 AUIRA27TR
	44	18	100.0	520	14	CNS00R7E	AL086744 Arabidops
	45	18	100.0	521	14	CNS00NZ5	AL082559 Arabidops
	46	18	100.0	522	11	BH244760	BH244760 AUIJA68TR
c	47	18	100.0	524	11	BH243951	BH243951 AUIRD63TR
	48	18	100.0	527	3	BQ851421	BQ851421 QGB15E20.
c	49	18	100.0	528	11	BH244809	BH244809 AUIJA24TF
	50	18	100.0	537	11	BH235380	BH235380 AUIVA05TR
	51	18	100.0	543	14	CNS00NS4	AL082306 Arabidops
	52	18	100.0	552	11	BH236544	BH236544 AUJFA64TF
c	53	18	100.0	556	11	BH243699	BH243699 AUIRA19TF

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549960&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	600	100.0	600	2	AR264380	AR264380 Sequence
2	600	100.0	600	2	AR494855	AR494855 Sequence
3	600	100.0	600	2	AR779195	AR779195 Sequence
4	600	100.0	12286	2	AR264383	AR264383 Sequence
5	600	100.0	12286	2	AR494858	AR494858 Sequence
6	600	100.0	12286	2	AR779198	AR779198 Sequence
7	571.2	95.2	4609	2	AR264386	AR264386 Sequence
8	571.2	95.2	4609	2	AR494861	AR494861 Sequence
9	571.2	95.2	4609	2	AR779201	AR779201 Sequence
10	571.2	95.2	8573	4	AF186184	AF186184 Glycine m
11	568.2	94.7	597	2	AR264399	AR264399 Sequence
12	568.2	94.7	597	2	AR494874	AR494874 Sequence
13	568.2	94.7	597	2	AR779214	AR779214 Sequence
14	532	88.7	9829	2	AR264384	AR264384 Sequence
15	532	88.7	9829	2	AR494859	AR494859 Sequence
16	532	88.7	9829	2	AR779199	AR779199 Sequence
17	532	88.7	10128	4	AF186182	AF186182 Glycine m
18	529.6	88.3	762	2	AR494934	AR494934 Sequence
19	529.6	88.3	762	2	AR779274	AR779274 Sequence
20	529.6	88.3	762	4	AF378068	AF378068 Glycine m
21	526.4	87.7	762	2	AR494928	AR494928 Sequence
22	526.4	87.7	762	2	AR779268	AR779268 Sequence
23	526.4	87.7	762	4	AF378062	AF378062 Glycine m
24	523.2	87.2	12571	2	AR264385	AR264385 Sequence
25	523.2	87.2	12571	2	AR494860	AR494860 Sequence
26	523.2	87.2	12571	2	AR779200	AR779200 Sequence
27	523.2	87.2	12886	4	AF186183	AF186183 Glycine m
28	502.6	83.8	763	2	AR494929	AR494929 Sequence
29	502.6	83.8	763	2	AR779269	AR779269 Sequence
30	502.6	83.8	763	4	AF378063	AF378063 Glycine m
31	430	71.7	762	2	AR494930	AR494930 Sequence
32	430	71.7	762	2	AR779270	AR779270 Sequence
33	430	71.7	762	4	AF378064	AF378064 Glycine m
c 34	360.6	60.1	86045	12	AP007813	AP007813 Lotus cor
35	360.6	60.1	155108	12	AP007528	AP007528 Lotus cor
36	359	59.8	92281	4	AP004896	AP004896 Lotus cor
37	352.6	58.8	762	2	AR494938	AR494938 Sequence
38	352.6	58.8	762	2	AR779278	AR779278 Sequence
39	352.6	58.8	762	4	AF378072	AF378072 Glycine m
40	351.6	58.6	762	2	AR494936	AR494936 Sequence
41	351.6	58.6	762	2	AR779276	AR779276 Sequence
42	351.6	58.6	762	4	AF378070	AF378070 Glycine m
43	350.2	58.4	125364	12	AC175087	AC175087 Glycine t
44	349.8	58.3	761	2	AR494939	AR494939 Sequence
45	349.8	58.3	761	2	AR779279	AR779279 Sequence

ALIGNMENTS

RESULT 1
AR264380

SCORE Search Results Details for Application 10 and Search Result us-10-615-005-11.rng

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:
[start](#)

[Go Bac](#)

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 07:26:47 ; Search time 488.488 Seconds
(without alignments)
8563.880 Million cell updates/sec

Title: US-10-615-005-11
Perfect score: 600
Sequence: 1 ttggaggctgggctcatata.....tcctaggccacaagatctca 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	600	100.0	600	3	AAZ35258	Aaz35258 Plant ret
2	600	100.0	12286	3	AAZ35261	Aaz35261 Plant gen
3	571.2	95.2	4609	3	AAZ35273	Aaz35273 Soybean r
4	568.2	94.7	597	3	AAZ35280	Aaz35280 Soybean r
5	532	88.7	9829	3	AAZ35271	Aaz35271 Soybean r
6	523.2	87.2	12571	3	AAZ35272	Aaz35272 Soybean r
7	345.6	57.6	9139	3	AAZ35274	Aaz35274 Soybean r
8	313.8	52.3	597	3	AAZ35266	Aaz35266 Pea retro
9	307.8	51.3	82138	3	AAF22305_10	Continuation (11 o
c 10	307.8	51.3	94895	3	AAF22302	Aaf22302 BAC conta
11	304.6	50.8	600	3	AAZ35264	Aaz35264 Arabidops
12	304.6	50.8	1791	10	ADJ81516	Adj81516 Plant ret
13	304.6	50.8	13894	10	ADJ81499	Adj81499 Plant ret
14	304.6	50.8	13966	10	ADJ81500	Adj81500 Plant ret
c 15	304.6	50.8	59590	3	AAF22281	Aaf22281 BAC conta
16	303	50.5	14016	10	ADJ81505	Adj81505 Plant ret
c 17	303	50.5	82138	3	AAF22305_10	Continuation (11 o
18	303	50.5	83390	3	AAF22283	Aaf22283 BAC conta
19	303	50.5	90336	3	AAF22289	Aaf22289 BAC conta
20	303	50.5	94895	3	AAF22302	Aaf22302 BAC conta
c 21	303	50.5	103929	3	AAF22287	Aaf22287 BAC conta
c 22	303	50.5	134499	3	AAF22286	Aaf22286 BAC conta
23	301.4	50.2	79122	3	AAF22294	Aaf22294 BAC conta
24	300	50.0	92584	3	AAF22288	Aaf22288 BAC conta
25	299.8	50.0	13938	10	ADJ81503	Adj81503 Plant ret
26	299.8	50.0	14005	10	ADJ81504	Adj81504 Plant ret
27	295.8	49.3	129021	3	AAF22296	Aaf22296 BAC conta
28	295	49.2	163319	3	AAF22306	Aaf22306 Arabidops
c 29	291.4	48.6	64415	3	AAF22279	Aaf22279 BAC conta
30	290.8	48.5	13320	10	ADJ81502	Adj81502 Plant ret
31	287.8	48.0	64415	3	AAF22279	Aaf22279 BAC conta
c 32	287	47.8	109973	3	AAF22298	Aaf22298 BAC conta
33	286.6	47.8	13868	10	ADJ81501	Adj81501 Plant ret
c 34	274.2	45.7	110000	3	AAF22303_0	Aaf22303 Arabidops
c 35	273.4	45.6	40349	3	AAF22278	Aaf22278 BAC conta
c 36	272	45.3	96988	3	AAF22290	Aaf22290 BAC conta
37	268.8	44.8	110000	3	AAF22305_08	Continuation (9 of
38	264.6	44.1	110000	3	AAF22305_09	Continuation (10 o
39	251.6	41.9	80450	3	AAF22295	Aaf22295 BAC conta
c 40	181.2	30.2	110000	3	AAF22303_1	Continuation (2 of
41	172.4	28.7	10482	3	AAZ35275	Aaz35275 Soybean r
42	159.2	26.5	109973	3	AAF22298	Aaf22298 BAC conta
c 43	104.2	17.4	76363	8	ACF30938	Acf30938 Rice cult
c 44	104.2	17.4	76363	12	ADI09997	Adi09997 Rice cult
c 45	104.2	17.4	76363	12	ADK72433	Adk72433 Rice fert

ALIGNMENTS

RESULT 1

AAZ35258

ID AAZ35258 standard; DNA; 600 BP.

XX

AC AAZ35258;

XX

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 11.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-11.rnpbm.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:36:14 ; Search time 1075.62 Seconds
(without alignments)
6854.257 Million cell updates/sec

Title: US-10-615-005-11
Perfect score: 600
Sequence: 1 ttggaggctgggctcatata.....tcctaggccacaagatctca 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	600	100.0	600	3	US-09-965-553-11	Sequence 11, Appl
2	600	100.0	600	8	US-10-615-005-11	Sequence 11, Appl
3	600	100.0	600	8	US-10-395-607-11	Sequence 11, Appl
4	600	100.0	600	8	US-10-799-870-11	Sequence 11, Appl
5	600	100.0	12286	3	US-09-965-553-17	Sequence 17, Appl
6	600	100.0	12286	8	US-10-615-005-17	Sequence 17, Appl
7	600	100.0	12286	8	US-10-395-607-17	Sequence 17, Appl
8	600	100.0	12286	8	US-10-799-870-17	Sequence 17, Appl
9	571.2	95.2	4609	3	US-09-965-553-21	Sequence 21, Appl
10	571.2	95.2	4609	8	US-10-615-005-21	Sequence 21, Appl
11	571.2	95.2	4609	8	US-10-395-607-21	Sequence 21, Appl
12	571.2	95.2	4609	8	US-10-799-870-21	Sequence 21, Appl
13	568.2	94.7	597	3	US-09-965-553-34	Sequence 34, Appl
14	568.2	94.7	597	8	US-10-615-005-34	Sequence 34, Appl
15	568.2	94.7	597	8	US-10-395-607-34	Sequence 34, Appl
16	568.2	94.7	597	8	US-10-799-870-34	Sequence 34, Appl
17	532	88.7	9829	3	US-09-965-553-19	Sequence 19, Appl
18	532	88.7	9829	8	US-10-615-005-19	Sequence 19, Appl
19	532	88.7	9829	8	US-10-395-607-19	Sequence 19, Appl
20	532	88.7	9829	8	US-10-799-870-19	Sequence 19, Appl
21	529.6	88.3	762	8	US-10-395-607-148	Sequence 148, App
22	529.6	88.3	762	8	US-10-799-870-148	Sequence 148, App
23	526.4	87.7	762	8	US-10-395-607-136	Sequence 136, App
24	526.4	87.7	762	8	US-10-799-870-136	Sequence 136, App
25	523.2	87.2	12571	3	US-09-965-553-20	Sequence 20, Appl
26	523.2	87.2	12571	8	US-10-615-005-20	Sequence 20, Appl
27	523.2	87.2	12571	8	US-10-395-607-20	Sequence 20, Appl
28	523.2	87.2	12571	8	US-10-799-870-20	Sequence 20, Appl
29	502.6	83.8	763	8	US-10-395-607-138	Sequence 138, App
30	502.6	83.8	763	8	US-10-799-870-138	Sequence 138, App
31	430	71.7	762	8	US-10-395-607-140	Sequence 140, App
32	430	71.7	762	8	US-10-799-870-140	Sequence 140, App
33	356.4	59.4	4651	8	US-10-424-599-96404	Sequence 96404, A
34	352.6	58.8	762	8	US-10-395-607-156	Sequence 156, App
35	352.6	58.8	762	8	US-10-799-870-156	Sequence 156, App
36	351.6	58.6	762	8	US-10-395-607-152	Sequence 152, App
37	351.6	58.6	762	8	US-10-799-870-152	Sequence 152, App
38	349.8	58.3	761	8	US-10-395-607-158	Sequence 158, App
39	349.8	58.3	761	8	US-10-799-870-158	Sequence 158, App
40	348.8	58.1	761	8	US-10-395-607-150	Sequence 150, App
41	348.8	58.1	761	8	US-10-799-870-150	Sequence 150, App
42	345.6	57.6	9139	3	US-09-965-553-22	Sequence 22, Appl
43	345.6	57.6	9139	8	US-10-615-005-22	Sequence 22, Appl
44	345.6	57.6	9139	8	US-10-395-607-22	Sequence 22, Appl
45	345.6	57.6	9139	8	US-10-799-870-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

No.	Score	Match	Length	DB	ID	Description
1	159.4	26.6	1738	6	US-10-449-902-7359	Sequence 7359, Ap
2	108	18.0	3732	6	US-10-449-902-12764	Sequence 12764, A
3	92.8	15.5	2174	6	US-10-953-349-39530	Sequence 39530, A
4	92.2	15.4	3020	6	US-10-953-349-37705	Sequence 37705, A
5	90.6	15.1	1604	6	US-10-449-902-7056	Sequence 7056, Ap
6	90.6	15.1	2122	6	US-10-953-349-37241	Sequence 37241, A
7	86.2	14.4	2092	6	US-10-449-902-9257	Sequence 9257, Ap
8	86.2	14.4	3434	6	US-10-449-902-15788	Sequence 15788, A
9	82.4	13.7	4498	7	US-11-217-529-190990	Sequence 190990,
10	80.4	13.4	2930	6	US-10-449-902-16763	Sequence 16763, A
11	78.8	13.1	4187	6	US-10-449-902-18580	Sequence 18580, A
12	76.2	12.7	3066	6	US-10-449-902-196	Sequence 196, App
13	76.2	12.7	4559	6	US-10-449-902-17469	Sequence 17469, A
14	76.2	12.7	5050	6	US-10-449-902-28374	Sequence 28374, A
c 15	70.4	11.7	1174	6	US-10-449-902-5570	Sequence 5570, Ap
c 16	68	11.3	1876	6	US-10-953-349-38211	Sequence 38211, A
17	65.6	10.9	1838	6	US-10-449-902-24362	Sequence 24362, A
18	53.8	9.0	2771	6	US-10-449-902-8893	Sequence 8893, Ap
19	48.2	8.0	858	6	US-10-953-349-37957	Sequence 37957, A
20	40.8	6.8	1793	6	US-10-449-902-9892	Sequence 9892, Ap
c 21	34.6	5.8	1758	7	US-11-217-529-1069	Sequence 1069, Ap
22	33	5.5	2406	7	US-11-266-748A-26169	Sequence 26169, A
c 23	32.6	5.4	2988	7	US-11-293-697-584	Sequence 584, App
24	32	5.3	2556	7	US-11-217-529-496	Sequence 496, App
25	31.8	5.3	906	6	US-10-449-902-13898	Sequence 13898, A
26	31.6	5.3	538	7	US-11-266-748A-274175	Sequence 274175,
c 27	31.6	5.3	538	7	US-11-266-748A-334692	Sequence 334692,
28	30.6	5.1	755217	7	US-11-266-748A-29045	Sequence 29045, A
29	30.4	5.1	2979	6	US-10-449-902-18549	Sequence 18549, A
c 30	30.4	5.1	294540	7	US-11-266-748A-23953	Sequence 23953, A
31	30.2	5.0	643	7	US-11-266-748A-13999	Sequence 13999, A
c 32	30.2	5.0	1014	7	US-11-217-529-81874	Sequence 81874, A
33	30.2	5.0	1139	7	US-11-266-748A-262527	Sequence 262527,
c 34	30.2	5.0	1139	7	US-11-266-748A-323044	Sequence 323044,
35	30.2	5.0	1276	7	US-11-266-748A-348273	Sequence 348273,
36	30.2	5.0	1276	7	US-11-266-748A-381717	Sequence 381717,
c 37	30.2	5.0	1276	7	US-11-266-748A-431652	Sequence 431652,
38	30.2	5.0	1663	7	US-11-266-748A-85235	Sequence 85235, A
c 39	30.2	5.0	1663	7	US-11-266-748A-138046	Sequence 138046,
40	30.2	5.0	1857	6	US-10-449-902-3474	Sequence 3474, Ap
c 41	30.2	5.0	2603	7	US-11-266-748A-355218	Sequence 355218,
c 42	30.2	5.0	2603	7	US-11-266-748A-385209	Sequence 385209,
43	30.2	5.0	2603	7	US-11-266-748A-438597	Sequence 438597,
44	30	5.0	718	7	US-11-266-748A-297697	Sequence 297697,
45	30	5.0	4242	7	US-11-217-529-6100	Sequence 6100, Ap

ALIGNMENTS

RESULT 1

US-10-449-902-7359

; Sequence 7359, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549965&ItemName=... 8/17/2006

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
c 1	512	85.3	929	12	CG823174
					CG823174 SOYDE90TH
2	508.8	84.8	922	13	CZ512661
					CZ512661 GMW2-65L1
3	449.2	74.9	909	13	CZ514713
					CZ514713 GMW2-78F2
c 4	395	65.8	926	13	CZ525914
					CZ525914 GMW2-90H1
c 5	391.6	65.3	845	14	DU645726
					DU645726 gmp1-138a
c 6	366.8	61.1	933	13	CZ505263
					CZ505263 GMW2-16C1
c 7	345	57.5	921	13	CZ507681
					CZ507681 GMW2-39I1
8	338.6	56.4	683	14	CR319234
					CR319234 mte1-44D4
9	333.6	55.6	803	12	CG955544
					CG955544 MBEGN36TF
10	331.6	55.3	778	14	CR306153
					CR306153 mte1-26G1
c 11	331.4	55.2	919	13	CZ500310
					CZ500310 GMW2-5D24
c 12	330.6	55.1	623	14	DE239932
					DE239932 Trifolium
13	328.6	54.8	828	12	CG820169
					CG820169 SOYEB24TH
14	324.2	54.0	670	12	CC000397
					CC000397 pPGPseq-4
c 15	323.2	53.9	774	13	DU120492
					DU120492 KBrH107J1
c 16	322.6	53.8	931	13	CZ516117
					CZ516117 GMW2-49K6
c 17	322.2	53.7	820	13	DU123508
					DU123508 KBrH097M1
c 18	321.4	53.6	714	11	BZ021183
					BZ021183 oeh01g01.
c 19	317.4	52.9	959	14	CT019028
					CT019028 KBrH127L1
c 20	317	52.8	582	11	BH421575
					BH421575 BOHEX22TF
21	315.2	52.5	697	11	BZ087809
					BZ087809 lki22c03.
c 22	315.2	52.5	727	11	BH423185
					BH423185 BOHHA57TR
c 23	315.2	52.5	841	11	BH718174
					BH718174 BOMGI87TF
24	315.2	52.5	911	13	CZ503425
					CZ503425 GMW2-14N2
25	314.2	52.4	700	14	CR312031
					CR312031 mte1-34M1
c 26	313.6	52.3	856	14	DU984250
					DU984250 KBrH1074E
27	313.6	52.3	981	11	BZ495499
					BZ495499 BONKN79TR
c 28	313.4	52.2	836	14	CT015708
					CT015708 KBrH124D0
29	311	51.8	693	12	CC951746
					CC951746 BOICL36TR
c 30	311	51.8	695	11	BH952205
					BH952205 odh78f09.
c 31	310.4	51.7	759	11	BH655348
					BH655348 BOMEL58TR
c 32	310.4	51.7	834	11	BH435343
					BH435343 BOHAU19TF
c 33	310.4	51.7	999	11	BZ456544
					BZ456544 BONEA18TF
34	309.2	51.5	807	11	BZ484101
					BZ484101 BONEZ50TR
c 35	308.8	51.5	712	11	BZ022306
					BZ022306 oeg94h08.
c 36	308.8	51.5	734	11	BZ509680
					BZ509680 BOMQV36TR
37	308.8	51.5	762	11	BH497441
					BH497441 BOHBD63TR
38	308.8	51.5	822	13	DU102154
					DU102154 JBnY026E1
c 39	307.6	51.3	842	11	BH448511
					BH448511 BOGOM52TF
c 40	307.2	51.2	688	11	BH992513
					BH992513 oeg79e11.
41	307.2	51.2	768	11	BH714463
					BH714463 BOMPQ54TR
42	307.2	51.2	814	11	BH697068
					BH697068 BOMOT46TR
c 43	307.2	51.2	930	14	DU899002
					DU899002 411599 To
44	306.6	51.1	886	13	DU107133
					DU107133 JBnY040B0
c 45	305.6	50.9	834	11	BZ433352
					BZ433352 BONNE92TF

ALIGNMENTS

RESULT 1

CG823174/c

LOCUS CG823174 929 bp DNA linear GSS 18-NOV-2003

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 15.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-15.rge.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 07:33:17 ; Search time 1233.34 Seconds
(without alignments)
9955.034 Million cell updates/sec

Title: US-10-615-005-15
Perfect score: 192
Sequence: 1 tttgaactaatgtgtgatgc.....tcagggtcatacttgataggg 192

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	192	100.0	192	2	AR264382	AR264382 Sequence
2	192	100.0	192	2	AR494857	AR494857 Sequence
3	192	100.0	192	2	AR779197	AR779197 Sequence
4	192	100.0	12286	2	AR264383	AR264383 Sequence
5	192	100.0	12286	2	AR494858	AR494858 Sequence
6	192	100.0	12286	2	AR779198	AR779198 Sequence
7	182.4	95.0	4609	2	AR264386	AR264386 Sequence
8	182.4	95.0	4609	2	AR494861	AR494861 Sequence
9	182.4	95.0	4609	2	AR779201	AR779201 Sequence
10	182.4	95.0	8573	4	AF186184	AF186184 Glycine m
11	177.6	92.5	12571	2	AR264385	AR264385 Sequence
12	177.6	92.5	12571	2	AR494860	AR494860 Sequence
13	177.6	92.5	12571	2	AR779200	AR779200 Sequence
14	177.6	92.5	12886	4	AF186183	AF186183 Glycine m
15	171.2	89.2	9829	2	AR264384	AR264384 Sequence
16	171.2	89.2	9829	2	AR494859	AR494859 Sequence
17	171.2	89.2	9829	2	AR779199	AR779199 Sequence
18	171.2	89.2	10128	4	AF186182	AF186182 Glycine m
c 19	125.4	65.3	121681	12	AC167785	AC167785 Glycine m
20	125.4	65.3	147462	12	AC174437	AC174437 Teramnus
c 21	123.8	64.5	86045	12	AP007813	AP007813 Lotus cor
22	123.8	64.5	92281	4	AP004896	AP004896 Lotus cor
23	123.8	64.5	155108	12	AP007528	AP007528 Lotus cor
24	122.2	63.6	84894	12	AP007552	AP007552 Lotus cor
25	118.4	61.7	79604	12	AC166911	AC166911 Glycine t
c 26	115.8	60.3	76165	12	AP007510	AP007510 Lotus cor
c 27	115.8	60.3	112406	4	AP002062	AP002062 Arabidops
28	115.8	60.3	125328	12	AP007941	AP007941 Lotus cor
29	115.8	60.3	125364	12	AC175087	AC175087 Glycine t
c 30	115.4	60.1	173646	12	AC172299	AC172299 Glycine m
31	114.2	59.5	192	2	AR264398	AR264398 Sequence
32	114.2	59.5	192	2	AR494873	AR494873 Sequence
33	114.2	59.5	192	2	AR779213	AR779213 Sequence
34	114.2	59.5	10482	2	AR264388	AR264388 Sequence
35	114.2	59.5	10482	2	AR494863	AR494863 Sequence
36	114.2	59.5	10482	2	AR779203	AR779203 Sequence
37	114.2	59.5	10510	4	AF186186	AF186186 Glycine m
38	114.2	59.5	186482	12	AC172298	AC172298 Glycine m
39	112.6	58.6	9139	2	AR264387	AR264387 Sequence
40	112.6	58.6	9139	2	AR494862	AR494862 Sequence
41	112.6	58.6	9139	2	AR779202	AR779202 Sequence
42	112.6	58.6	13637	4	AF186185	AF186185 Glycine m
c 43	112.6	58.6	51248	4	AB046437	AB046437 Arabidops
44	112.6	58.6	94342	4	ATF4M19	AL356013 Arabidops
45	112.6	58.6	97397	4	AB073156	AB073156 Arabidops

ALIGNMENTS

RESULT 1
AR264382

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-15.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-15.rng.

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OM nucleic - nucleic search, using sw model

```
Run on:      June 29, 2006, 07:26:47 ; Search time 156.316 Seconds
              (without alignments)
              8563.880 Million cell updates/sec
```

```
Title:          US-10-615-005-15
Perfect score: 192
Sequence:      1 tttgaactaatgtgtgatgc.....tcaggtcataacttgataggg 192
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	177.6	92.5	12571	3	AAZ35272	Aaz35272 Soybean r
5	171.2	89.2	9829	3	AAZ35271	Aaz35271 Soybean r
6	114.2	59.5	192	3	AAZ35279	Aaz35279 Soybean r
7	114.2	59.5	10482	3	AAZ35275	Aaz35275 Soybean r
8	112.6	58.6	9139	3	AAZ35274	Aaz35274 Soybean r
c 9	109.4	57.0	109973	3	AAF22298	Aaf22298 BAC conta
10	107.2	55.8	192	3	AAZ35267	Aaz35267 Pea retro
11	104.6	54.5	92584	3	AAF22288	Aaf22288 BAC conta
12	103	53.6	13938	10	ADJ81503	Adj81503 Plant ret
13	103	53.6	14005	10	ADJ81504	Adj81504 Plant ret
14	103	53.6	79122	3	AAF22294	Aaf22294 BAC conta
15	101.4	52.8	192	3	AAZ35265	Aaz35265 Arabidops
16	101.4	52.8	1791	10	ADJ81516	Adj81516 Plant ret
17	101.4	52.8	13868	10	ADJ81501	Adj81501 Plant ret
18	101.4	52.8	13894	10	ADJ81499	Adj81499 Plant ret
19	101.4	52.8	13966	10	ADJ81500	Adj81500 Plant ret
20	101.4	52.8	14016	10	ADJ81505	Adj81505 Plant ret
21	101.4	52.8	64415	3	AAF22279	Aaf22279 BAC conta
22	99.8	52.0	13320	10	ADJ81502	Adj81502 Plant ret
c 23	98.2	51.1	82138	3	AAF22305_10	Continuation (11 o
24	98.2	51.1	94895	3	AAF22302	Aaf22302 BAC conta
c 25	95	49.5	59590	3	AAF22281	Aaf22281 BAC conta
26	95	49.5	83390	3	AAF22283	Aaf22283 BAC conta
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c 32	90.2	47.0	94895	3	AAF22302	Aaf22302 BAC conta
33	88.6	46.1	82138	3	AAF22305_10	Continuation (11 o
34	87.4	45.5	129021	3	AAF22296	Aaf22296 BAC conta
35	86.2	44.9	163319	3	AAF22306	Aaf22306 Arabidops
36	86	44.8	109973	3	AAF22298	Aaf22298 BAC conta
c 37	83	43.2	40349	3	AAF22278	Aaf22278 BAC conta
c 38	83	43.2	110000	3	AAF22303_0	Aaf22303 Arabidops
c 39	78.4	40.8	103929	3	AAF22287	Aaf22287 BAC conta
c 40	78.4	40.8	134499	3	AAF22286	Aaf22286 BAC conta
41	76.2	39.7	80450	3	AAF22295	Aaf22295 BAC conta
c 42	69.6	36.2	96988	3	AAF22290	Aaf22290 BAC conta
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ALIGNMENTS

RESULT 1
AAZ35260

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 15.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-15.rni.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:22:58 ; Search time 46.3025 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	192	100.0	192	3	US-09-586-106D-15	Sequence 15, Appl
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7	182.4	95.0	4609	3	US-09-322-478-21	Sequence 21, Appl
8	182.4	95.0	4609	3	US-09-586-106D-21	Sequence 21, Appl
9	182.4	95.0	4609	3	US-10-799-870-21	Sequence 21, Appl
10	177.6	92.5	12571	3	US-09-322-478-20	Sequence 20, Appl
11	177.6	92.5	12571	3	US-09-586-106D-20	Sequence 20, Appl
12	177.6	92.5	12571	3	US-10-799-870-20	Sequence 20, Appl
13	171.2	89.2	9829	3	US-09-322-478-19	Sequence 19, Appl
14	171.2	89.2	9829	3	US-09-586-106D-19	Sequence 19, Appl
15	171.2	89.2	9829	3	US-10-799-870-19	Sequence 19, Appl
16	114.2	59.5	192	3	US-09-322-478-33	Sequence 33, Appl
17	114.2	59.5	192	3	US-09-586-106D-33	Sequence 33, Appl
18	114.2	59.5	192	3	US-10-799-870-33	Sequence 33, Appl
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20	114.2	59.5	10482	3	US-09-586-106D-23	Sequence 23, Appl
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ALIGNMENTS

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; Sequence 15, Application US/09322478

; Patent No. 6331662

; GENERAL INFORMATION:

; APPLICANT: Wright, David A.

; APPLICANT: Voytas, Daniel F.

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6	192	100.0	12286	8	US-10-615-005-17	Sequence 17, Appl
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9	182.4	95.0	4609	3	US-09-965-553-21	Sequence 21, Appl
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42	103	53.6	3111	8	US-10-437-963-23928	Sequence 23928, A
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ALIGNMENTS

RESULT 1

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 15.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-15.rnpbm.

[start](#)

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26	114.2	59.5	10482	3	US-09-965-553-23	Sequence 23, Appl
27	114.2	59.5	10482	8	US-10-615-005-23	Sequence 23, Appl
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c 34	109.4	57.0	109974	15	US-11-117-187-204	Sequence 204, App
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37	107.2	55.8	192	8	US-10-395-607-30	Sequence 30, Appl
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ALIGNMENTS

RESULT 1

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-15.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-15.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:51:49 ; Search time 28.8939 Seconds
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Maximum Match 100%
Listing first 45 summaries

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- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
c 1	84.2	43.9	1738	6	US-10-449-902-7359	Sequence 7359, Ap
c 2	35.2	18.3	1000	7	US-11-266-748A-204623	Sequence 204623,
c 3	33.6	17.5	2418	6	US-10-449-902-21884	Sequence 21884, A
c 4	30.8	16.0	1072	6	US-10-953-349-26278	Sequence 26278, A
c 5	30.4	15.8	538	7	US-11-266-748A-379574	Sequence 379574,
c 6	30.4	15.8	538	7	US-11-266-748A-462953	Sequence 462953,
c 7	30.4	15.8	539	7	US-11-266-748A-213007	Sequence 213007,
c 8	30.4	15.8	539	7	US-11-266-748A-236242	Sequence 236242,
c 9	30.4	15.8	956	7	US-11-266-748A-249518	Sequence 249518,
c 10	30.4	15.8	1792	7	US-11-266-748A-32056	Sequence 32056, A
c 11	30.4	15.8	1792	7	US-11-266-748A-59804	Sequence 59804, A
c 12	29.4	15.3	1440	7	US-11-217-529-78747	Sequence 78747, A
c 13	29.4	15.3	2410	6	US-10-449-902-14265	Sequence 14265, A
c 14	29.4	15.3	2808	7	US-11-217-529-77371	Sequence 77371, A
c 15	29	15.1	533	7	US-11-266-748A-175830	Sequence 175830,
c 16	29	15.1	122638	7	US-11-266-748A-22259	Sequence 22259, A
c 17	28.8	15.0	815	7	US-11-266-748A-264629	Sequence 264629,
c 18	28.8	15.0	815	7	US-11-266-748A-325146	Sequence 325146,
c 19	28.8	15.0	815	7	US-11-266-748A-370467	Sequence 370467,
c 20	28.8	15.0	815	7	US-11-266-748A-453846	Sequence 453846,
c 21	28.8	15.0	1225	7	US-11-266-748A-368842	Sequence 368842,
c 22	28.8	15.0	1225	7	US-11-266-748A-452221	Sequence 452221,
c 23	28.8	15.0	1852	7	US-11-266-748A-183535	Sequence 183535,
c 24	28.8	15.0	261789	7	US-11-260-842-1	Sequence 1, Appli
c 25	28.6	14.9	1000	7	US-11-266-748A-197044	Sequence 197044,
c 26	28.6	14.9	2488	6	US-10-449-902-14868	Sequence 14868, A
c 27	28.4	14.8	1000	7	US-11-266-748A-118960	Sequence 118960,
c 28	28.4	14.8	1000	7	US-11-266-748A-161124	Sequence 161124,
c 29	28.4	14.8	1000	7	US-11-266-748A-194988	Sequence 194988,
c 30	28.4	14.8	1000	7	US-11-266-748A-293824	Sequence 293824,
c 31	28.4	14.8	1000	7	US-11-266-748A-345253	Sequence 345253,
c 32	28.4	14.8	1000	7	US-11-266-748A-405965	Sequence 405965,
c 33	28.4	14.8	1000	7	US-11-266-748A-477011	Sequence 477011,
c 34	28.4	14.8	1080	7	US-11-266-748A-188470	Sequence 188470,
c 35	28.4	14.8	1135	6	US-10-953-349-31185	Sequence 31185, A
c 36	28.4	14.8	1378	7	US-11-266-748A-80525	Sequence 80525, A
c 37	28.4	14.8	1378	7	US-11-266-748A-133336	Sequence 133336,
c 38	28.4	14.8	1561	7	US-11-266-748A-20584	Sequence 20584, A
c 39	28.4	14.8	1561	7	US-11-266-748A-62511	Sequence 62511, A
c 40	28.4	14.8	1561	7	US-11-266-748A-65350	Sequence 65350, A
c 41	28.4	14.8	7556	7	US-11-266-748A-30767	Sequence 30767, A
c 42	28.4	14.8	7556	7	US-11-266-748A-57498	Sequence 57498, A
c 43	28.4	14.8	142707	7	US-11-266-748A-24186	Sequence 24186, A
c 44	28.2	14.7	494	7	US-11-266-748A-269258	Sequence 269258,
c 45	28.2	14.7	494	7	US-11-266-748A-329775	Sequence 329775,

ALIGNMENTS

RESULT 1

US-10-449-902-7359

; Sequence 7359, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	172.8	90.0	485	13	CL881511	CL881511 abf51e02.
c	2	163.2	85.0	919	13	CZ522271	CZ522271 GMW2-82E7
	3	160.6	83.6	494	13	CL887536	CL887536 abf84f11.
	4	151	78.6	928	13	CZ521989	CZ521989 GMW2-81J1
c	5	147.2	76.7	783	12	CG824857	CG824857 SOYAM81TV
	6	139.8	72.8	937	13	CZ518879	CZ518879 GMW2-68K1
c	7	139.2	72.5	901	12	CG821980	CG821980 SOYEU16TV
c	8	139.2	72.5	916	13	CZ524331	CZ524331 GMW2-65H1
c	9	139.2	72.5	930	12	CG818993	CG818993 SOYAC75TV
	10	136.6	71.1	917	13	CZ515255	CZ515255 GMW2-83K6
	11	136.6	71.1	920	13	CZ500484	CZ500484 GMW2-13I1
	12	134.4	70.0	437	13	CL884362	CL884362 abf66f12.
c	13	133.4	69.5	932	13	CZ511907	CZ511907 GMW2-39L2
	14	131.8	68.6	924	13	CZ525808	CZ525808 GMW2-88P4
	15	127.6	66.5	614	11	AZ044562	AZ044562 Gm_UMB001
c	16	123.8	64.5	693	11	BZ038034	BZ038034 oeh88e03.
	17	123.8	64.5	717	11	BZ476782	BZ476782 BONDO33TR
	18	122.2	63.6	687	12	CC961142	CC961142 BOIGK45TF
	19	122.2	63.6	776	11	BZ441393	BZ441393 BONJQ88TF
	20	122.2	63.6	848	11	BH482408	BH482408 BOHGA73TR
c	21	120.6	62.8	925	13	CZ509579	CZ509579 GMW2-68A2
	22	120	62.5	519	11	BH008489	BH008489 ef16c09.x
c	23	120	62.5	588	14	DX070219	DX070219 KBrB079I1
c	24	120	62.5	728	14	DX035720	DX035720 KBrB033O2
	25	120	62.5	758	13	DU118223	DU118223 KBrH096N1
	26	120	62.5	782	11	BH443321	BH443321 BOGZX64TR
c	27	120	62.5	889	14	DX025455	DX025455 KBrB020H0
c	28	120	62.5	943	14	DX082827	DX082827 KBrB096E0
	29	119	62.0	530	11	BH575562	BH575562 BOHOV68TF
	30	119	62.0	679	11	BH587615	BH587615 BOGEG70TF
	31	119	62.0	693	11	BH671950	BH671950 BOMJQ55TR
c	32	119	62.0	693	11	BH947113	BH947113 obv11e09.
	33	119	62.0	777	11	BZ506017	BZ506017 BONFZ68TF
	34	119	62.0	880	12	CG825989	CG825989 SOYEU72TV
	35	119	62.0	902	12	CG819474	CG819474 SOYAE32TV
	36	119	62.0	956	11	BZ485077	BZ485077 BONDY72TF
c	37	119	62.0	1029	11	BZ485086	BZ485086 BONDY72TR
c	38	118.4	61.7	527	14	DX026095	DX026095 KBrB021E1
	39	118.4	61.7	658	13	CW980587	CW980587 KBrH004O0
c	40	118.4	61.7	666	14	DX017374	DX017374 KBrB009N0
c	41	118.4	61.7	704	11	BZ062919	BZ062919 11c02a02.
c	42	118.4	61.7	727	14	DX016925	DX016925 KBrB009D2
	43	118.4	61.7	752	11	BZ063242	BZ063242 1kz69d11.
c	44	118.4	61.7	763	14	DX019793	DX019793 KBrB013A1
c	45	118.4	61.7	780	14	DX062256	DX062256 KBrB069A2

ALIGNMENTS

RESULT 1

CL881511

LOCUS CL881511 485 bp DNA linear GSS 30-AUG-2004

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549972&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	6	100.0	8	2	BD014077	BD014077 Oligonucleotide
	2	6	100.0	8	2	BD014116	BD014116 High-chim
	3	6	100.0	8	2	BD192539	BD192539 Compositi
	4	6	100.0	8	2	BD272011	BD272011 Multipart
	5	6	100.0	8	2	BD272113	BD272113 Fusogenic
	6	6	100.0	8	2	CQ828608	CQ828608 Sequence
	7	6	100.0	8	2	CQ828610	CQ828610 Sequence
	8	6	100.0	8	2	CQ829013	CQ829013 Sequence
	9	6	100.0	8	2	CQ829055	CQ829055 Sequence
	10	6	100.0	8	2	CQ891672	CQ891672 Sequence
	11	6	100.0	8	2	E17092	E17092 Rhizoctonia
	12	6	100.0	9	2	AX669026	AX669026 Sequence
	13	6	100.0	9	2	AX669058	AX669058 Sequence
c	14	6	100.0	9	2	AX815429	AX815429 Sequence
	15	6	100.0	10	2	A72419	A72419 Sequence 6
c	16	6	100.0	10	2	A72420	A72420 Sequence 7
	17	6	100.0	10	2	A80129	A80129 Sequence 6
c	18	6	100.0	10	2	A80130	A80130 Sequence 7
	19	6	100.0	10	2	A82122	A82122 Sequence 1
c	20	6	100.0	10	2	A82123	A82123 Sequence 2
c	21	6	100.0	10	2	AR016042	AR016042 Sequence
	22	6	100.0	10	2	AR030236	AR030236 Sequence
c	23	6	100.0	10	2	AR059203	AR059203 Sequence
	24	6	100.0	10	2	AR074218	AR074218 Sequence
	25	6	100.0	10	2	AR074238	AR074238 Sequence
	26	6	100.0	10	2	AR074311	AR074311 Sequence
c	27	6	100.0	10	2	AR075514	AR075514 Sequence
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c	29	6	100.0	10	2	AR161912	AR161912 Sequence
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	31	6	100.0	10	2	BD007870	BD007870 LPS activ
	32	6	100.0	10	2	BD083081	BD083081 Human mat
c	33	6	100.0	10	2	BD083117	BD083117 Human mat
	34	6	100.0	10	2	BD083232	BD083232 Human mat
	35	6	100.0	10	2	BD091189	BD091189 P53-induc
c	36	6	100.0	10	2	BD161286	BD161286 Human act
	37	6	100.0	10	2	BD161453	BD161453 Human act
c	38	6	100.0	10	2	BD166485	BD166485 Human liv
c	39	6	100.0	10	2	BD166507	BD166507 Human liv
c	40	6	100.0	10	2	BD166529	BD166529 Human liv
c	41	6	100.0	10	2	BD166812	BD166812 Human liv
c	42	6	100.0	10	2	BD167007	BD167007 Human liv
c	43	6	100.0	10	2	BD167030	BD167030 Human liv
c	44	6	100.0	10	2	BD167033	BD167033 Human liv
	45	6	100.0	10	2	BD167046	BD167046 Human liv
	46	6	100.0	10	2	BD167108	BD167108 Human liv
	47	6	100.0	10	2	BD167177	BD167177 Human liv
c	48	6	100.0	10	2	BD176153	BD176153 Mammalian
	49	6	100.0	10	2	BD190832	BD190832 G-rich ol
	50	6	100.0	10	2	BD238616	BD238616 Preparati
	51	6	100.0	10	2	BD239038	BD239038 Preparati
	52	6	100.0	10	2	BD239101	BD239101 Preparati

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549973&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	6	100.0	6	2	AAQ97988	Aaq97988 Peptide n
c	2	6	100.0	6	12	ADO05790	Ado05790 Telomere-
	3	6	100.0	8	2	AAQ73378	Aaq73378 Anti-HSV-
	4	6	100.0	8	2	AAQ97974	Aaq97974 Peptide n
	5	6	100.0	8	2	AAQ97991	Aaq97991 Peptide n
	6	6	100.0	8	2	AAT09573	Aat09573 3'-primer
c	7	6	100.0	8	2	AAT09369	Aat09369 5'-primer
	8	6	100.0	8	2	AAV28242	Aav28242 Antisense
	9	6	100.0	8	2	AAX18772	Aax18772 Target HI
	10	6	100.0	8	2	AAX23651	Aax23651 Deletion
	11	6	100.0	8	3	AAZ49372	Aaz49372 HIV gp120
c	12	6	100.0	8	10	ADE14149	Ade14149 Optineuri
	13	6	100.0	8	10	ADE13918	Ade13918 Optineuri
c	14	6	100.0	8	12	ADO05791	Ado05791 Telomere-
	15	6	100.0	8	12	ADQ30480	Adq30480 Human VR1
	16	6	100.0	8	12	ADQ30035	Adq30035 Rat VR1 e
	17	6	100.0	8	12	ADQ30438	Adq30438 Human VR1
	18	6	100.0	8	12	ADQ30033	Adq30033 Rat VR1 e
	19	6	100.0	9	6	ABQ72177	Abq72177 Zinc fing
	20	6	100.0	9	6	ABQ72209	Abq72209 Zinc fing
c	21	6	100.0	9	8	ABX50037	Abx50037 Telomere
	22	6	100.0	9	9	ADA64536	Ada64536 Zinc fing
	23	6	100.0	9	9	ADA64504	Ada64504 Zinc fing
c	24	6	100.0	9	10	ADE13983	Ade13983 Optineuri
	25	6	100.0	9	10	ADM23228	Adm23228 Synthetic
	26	6	100.0	9	11	ADM23196	Adm23196 Synthetic
	27	6	100.0	10	2	AAQ73361	Aaq73361 Anti-HSV-
	28	6	100.0	10	2	AAQ62000	Aaq62000 Guanine q
	29	6	100.0	10	2	AAQ61850	Aaq61850 HSV repli
	30	6	100.0	10	2	AAQ61905	Aaq61905 HSV repli
	31	6	100.0	10	2	AAQ64020	Aaq64020 16S rRNA
	32	6	100.0	10	2	AAT08734	Aat08734 U14snoRNA
	33	6	100.0	10	2	AAQ97980	Aaq97980 Peptide n
	34	6	100.0	10	2	AAT08758	Aat08758 U14snoRNA
c	35	6	100.0	10	2	AAQ93130	Aaq93130 Telomeras
	36	6	100.0	10	2	AAT36249	Aat36249 CD28 expr
	37	6	100.0	10	2	AAX90342	Aax90342 CD28 inhi
c	38	6	100.0	10	2	AAT66050	Aat66050 (dC-dA)n.
	39	6	100.0	10	2	AAT98862	Aat98862 Core-bind
	40	6	100.0	10	2	AAX04582	Aax04582 Inverted
c	41	6	100.0	10	2	AAX04583	Aax04583 Inverted
c	42	6	100.0	10	2	AAX99946	Aax99946 Human par
	43	6	100.0	10	2	AAX86264	Aax86264 SAGE tag
	44	6	100.0	10	3	AAZ78091	Aaz78091 Human den
	45	6	100.0	10	3	AAZ78417	Aaz78417 Human den
	46	6	100.0	10	3	AAZ78913	Aaz78913 Human den
c	47	6	100.0	10	3	AAZ79695	Aaz79695 Human den
	48	6	100.0	10	3	AAZ79704	Aaz79704 Human den
	49	6	100.0	10	3	AAZ78028	Aaz78028 Human den
	50	6	100.0	10	3	AAZ79186	Aaz79186 Human den
	51	6	100.0	10	3	AAZ79408	Aaz79408 Human den
	52	6	100.0	10	3	AAZ79146	Aaz79146 Human den

SCORE Search Results Details for Application 10 and Search Result us-10-615-005-3.rni.

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This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 09:07:39 ; Search time 38.75 Seconds
(without alignments)
289.720 Million cell updates/sec

Title: US-10-615-005-3
Perfect score: 6
Sequence: 1 ttgggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID		Description	

	1	6	100.0	6	2	US-08-381-097A-1	Sequence 1, Appli
c	2	6	100.0	6	2	US-08-381-097A-2	Sequence 2, Appli
	3	6	100.0	6	3	US-08-819-867-2	Sequence 2, Appli
	4	6	100.0	6	3	US-09-322-478-3	Sequence 3, Appli
	5	6	100.0	6	3	US-09-378-535-2	Sequence 2, Appli
	6	6	100.0	6	3	US-09-940-173A-7	Sequence 7, Appli
	7	6	100.0	6	3	US-09-730-893-7	Sequence 7, Appli
	8	6	100.0	6	3	US-09-586-106D-3	Sequence 3, Appli
	9	6	100.0	6	3	US-10-799-870-3	Sequence 3, Appli
	10	6	100.0	8	2	US-08-031-147A-54	Sequence 54, Appl
	11	6	100.0	8	2	US-08-470-129-1	Sequence 1, Appli
	12	6	100.0	8	3	US-08-729-598-9	Sequence 9, Appli
	13	6	100.0	8	3	US-08-851-843A-44	Sequence 44, Appl
	14	6	100.0	8	3	US-08-854-050-44	Sequence 44, Appl
	15	6	100.0	8	3	US-09-430-323-44	Sequence 44, Appl
	16	6	100.0	8	3	US-09-287-175-7	Sequence 7, Appli
	17	6	100.0	8	3	US-10-029-598-37	Sequence 37, Appl
	18	6	100.0	8	3	US-09-766-253-44	Sequence 44, Appl
	19	6	100.0	8	3	US-10-081-463-7	Sequence 7, Appli
	20	6	100.0	8	3	US-09-108-673A-104	Sequence 104, App
	21	6	100.0	8	3	US-10-054-295-44	Sequence 44, Appl
	22	6	100.0	8	3	US-09-438-486A-44	Sequence 44, Appl
	23	6	100.0	8	4	US-10-690-984-6	Sequence 6, Appli
	24	6	100.0	8	4	US-10-690-984-7	Sequence 7, Appli
	25	6	100.0	8	5	US-10-054-611-44	Sequence 44, Appl
	26	6	100.0	8	7	PCT-US94-02471-54	Sequence 54, Appl
	27	6	100.0	8	7	PCT-US96-08757A-17	Sequence 17, Appl
c	28	6	100.0	9	3	US-08-879-457-1	Sequence 1, Appli
c	29	6	100.0	9	3	US-08-819-867-1	Sequence 1, Appli
c	30	6	100.0	9	3	US-08-675-119-1	Sequence 1, Appli
	31	6	100.0	9	3	US-09-322-478-40	Sequence 40, Appl
c	32	6	100.0	9	3	US-09-378-535-1	Sequence 1, Appli
c	33	6	100.0	9	3	US-09-467-932-1	Sequence 1, Appli
	34	6	100.0	9	3	US-09-586-106D-40	Sequence 40, Appl
	35	6	100.0	9	3	US-10-799-870-40	Sequence 40, Appl
	36	6	100.0	9	5	US-09-990-186-2475	Sequence 2475, Ap
	37	6	100.0	9	5	US-09-990-186-2507	Sequence 2507, Ap
c	38	6	100.0	10	2	US-07-704-288C-24	Sequence 24, Appl
	39	6	100.0	10	2	US-08-031-147A-37	Sequence 37, Appl
c	40	6	100.0	10	2	US-08-222-177A-399	Sequence 399, App
c	41	6	100.0	10	2	US-08-330-123A-10	Sequence 10, Appl
c	42	6	100.0	10	2	US-08-379-259-24	Sequence 24, Appl
c	43	6	100.0	10	2	US-08-482-115B-10	Sequence 10, Appl
c	44	6	100.0	10	2	US-08-660-678A-10	Sequence 10, Appl
	45	6	100.0	10	2	US-08-590-571-47	Sequence 47, Appl
c	46	6	100.0	10	2	US-08-485-778-41	Sequence 41, Appl
	47	6	100.0	10	2	US-08-403-888A-26	Sequence 26, Appl
	48	6	100.0	10	2	US-08-403-888A-46	Sequence 46, Appl
	49	6	100.0	10	2	US-08-403-888A-119	Sequence 119, App
c	50	6	100.0	10	2	US-08-472-802C-11	Sequence 11, Appl
	51	6	100.0	10	3	US-08-819-867-69	Sequence 69, Appl
c	52	6	100.0	10	3	US-08-520-550A-41	Sequence 41, Appl
	53	6	100.0	10	3	US-09-069-434-16	Sequence 16, Appl
c	54	6	100.0	10	3	US-08-998-443-10	Sequence 10, Appl
	55	6	100.0	10	3	US-08-906-691-34	Sequence 34, Appl
c	56	6	100.0	10	3	US-08-434-099A-35	Sequence 35, Appl
c	57	6	100.0	10	3	US-09-060-523-10	Sequence 10, Appl
c	58	6	100.0	10	3	US-09-580-517-10	Sequence 10, Appl
	59	6	100.0	10	3	US-09-154-750A-67	Sequence 67, Appl
c	60	6	100.0	10	3	US-09-052-753B-12	Sequence 12, Appl
c	61	6	100.0	10	3	US-09-914-259-96	Sequence 96, Appl

SCORE Search Results Details for Application 10 Search Result us-10-615-005-3.rnpbn

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:
[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 09:14:25 ; Search time 312.25 Seconds
(without alignments)
236.111 Million cell updates/sec

Title: US-10-615-005-3
Perfect score: 6
Sequence: 1 ttggggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	6	100.0	6	3	US-09-730-893-7	Sequence 7, Appli
2	6	100.0	6	3	US-09-965-553-3	Sequence 3, Appli
3	6	100.0	6	3	US-09-940-173A-7	Sequence 7, Appli
4	6	100.0	6	7	US-10-336-265-39	Sequence 39, Appl
5	6	100.0	6	7	US-10-232-927A-2	Sequence 2, Appli
6	6	100.0	6	8	US-10-615-005-3	Sequence 3, Appli
7	6	100.0	6	8	US-10-395-607-3	Sequence 3, Appli
8	6	100.0	6	8	US-10-799-870-3	Sequence 3, Appli
9	6	100.0	6	9	US-10-775-818-7	Sequence 7, Appli
10	6	100.0	8	3	US-09-843-676-44	Sequence 44, Appl
11	6	100.0	8	3	US-09-766-253-44	Sequence 44, Appl
12	6	100.0	8	3	US-09-438-486-44	Sequence 44, Appl
13	6	100.0	8	3	US-09-876-549-5	Sequence 5, Appli
14	6	100.0	8	6	US-10-071-822A-7	Sequence 7, Appli
15	6	100.0	8	6	US-10-053-758-44	Sequence 44, Appl
16	6	100.0	8	6	US-10-029-598-37	Sequence 37, Appl
17	6	100.0	8	6	US-10-054-295-44	Sequence 44, Appl
18	6	100.0	8	6	US-10-054-611-44	Sequence 44, Appl
19	6	100.0	8	7	US-10-336-265-41	Sequence 41, Appl
20	6	100.0	8	7	US-10-091-281-29	Sequence 29, Appl
c 21	6	100.0	8	7	US-10-091-281-260	Sequence 260, App
22	6	100.0	8	9	US-10-793-497-37	Sequence 37, Appl
23	6	100.0	8	10	US-10-690-984-6	Sequence 6, Appli
24	6	100.0	8	10	US-10-690-984-7	Sequence 7, Appli
25	6	100.0	9	3	US-09-965-553-40	Sequence 40, Appl
26	6	100.0	9	3	US-09-990-186-2475	Sequence 2475, Ap
27	6	100.0	9	3	US-09-990-186-2507	Sequence 2507, Ap
28	6	100.0	9	3	US-09-989-994-2475	Sequence 2475, Ap
29	6	100.0	9	3	US-09-989-994-2507	Sequence 2507, Ap
30	6	100.0	9	3	US-09-876-549-3	Sequence 3, Appli
c 31	6	100.0	9	7	US-10-091-281-94	Sequence 94, Appl
c 32	6	100.0	9	7	US-10-232-927A-1	Sequence 1, Appli
33	6	100.0	9	8	US-10-615-005-40	Sequence 40, Appl
34	6	100.0	9	8	US-10-395-607-40	Sequence 40, Appl
35	6	100.0	9	8	US-10-799-870-40	Sequence 40, Appl
36	6	100.0	9	16	US-11-225-686-2475	Sequence 2475, Ap
37	6	100.0	9	16	US-11-225-686-2507	Sequence 2507, Ap
38	6	100.0	9	16	US-11-202-009-2475	Sequence 2475, Ap
39	6	100.0	9	16	US-11-202-009-2507	Sequence 2507, Ap
c 40	6	100.0	10	3	US-09-057-351-10	Sequence 10, Appl
41	6	100.0	10	3	US-09-154-750A-67	Sequence 67, Appl
42	6	100.0	10	3	US-09-907-279-3	Sequence 3, Appli
43	6	100.0	10	6	US-10-033-145-34	Sequence 34, Appl
44	6	100.0	10	6	US-10-033-145-456	Sequence 456, App
45	6	100.0	10	6	US-10-033-145-519	Sequence 519, App
c 46	6	100.0	10	6	US-10-033-145-689	Sequence 689, App
47	6	100.0	10	6	US-10-033-145-845	Sequence 845, App
48	6	100.0	10	6	US-10-033-145-1006	Sequence 1006, Ap
c 49	6	100.0	10	6	US-10-033-145-1229	Sequence 1229, Ap
50	6	100.0	10	6	US-10-033-145-1341	Sequence 1341, Ap
c 51	6	100.0	10	6	US-10-033-145-1345	Sequence 1345, Ap
52	6	100.0	10	6	US-10-033-145-1574	Sequence 1574, Ap
53	6	100.0	10	6	US-10-033-145-1614	Sequence 1614, Ap
54	6	100.0	10	6	US-10-033-145-1836	Sequence 1836, Ap
55	6	100.0	10	6	US-10-033-145-1850	Sequence 1850, Ap

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-3.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:005-3.rnpbn.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 09:33:22 ; Search time 272.75 Seconds
(without alignments)
26.013 Million cell updates/sec

Title: US-10-615-005-3
Perfect score: 6
Sequence: 1 ttgggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match Length	DB	ID	Description	
1	6	100.0	10	6	US-10-524-432-182	Sequence 182, App
2	6	100.0	10	6	US-10-524-432-559	Sequence 559, App
3	6	100.0	10	6	US-10-524-432-811	Sequence 811, App
4	6	100.0	10	7	US-11-287-053-8	Sequence 8, Appli
c 5	6	100.0	10	7	US-11-287-053-9	Sequence 9, Appli
6	6	100.0	10	7	US-11-287-053-10	Sequence 10, Appl
c 7	6	100.0	10	7	US-11-287-053-11	Sequence 11, Appl
8	6	100.0	10	7	US-11-287-053-12	Sequence 12, Appl
9	6	100.0	11	7	US-11-158-209-4	Sequence 4, Appli
10	6	100.0	11	7	US-11-158-209-10	Sequence 10, Appl
11	6	100.0	11	7	US-11-158-209-125	Sequence 125, App
c 12	6	100.0	11	7	US-11-158-209-184	Sequence 184, App
13	6	100.0	11	7	US-11-158-209-200	Sequence 200, App
c 14	6	100.0	11	7	US-11-158-209-265	Sequence 265, App
c 15	6	100.0	11	7	US-11-158-209-1028	Sequence 1028, Ap
c 16	6	100.0	11	7	US-11-158-209-1034	Sequence 1034, Ap
17	6	100.0	11	7	US-11-158-209-1320	Sequence 1320, Ap
c 18	6	100.0	12	7	US-11-212-812A-534	Sequence 534, App
c 19	6	100.0	16	6	US-10-517-441-219	Sequence 219, App
20	6	100.0	16	6	US-10-517-441-1587	Sequence 1587, Ap
21	6	100.0	16	6	US-10-517-441-1588	Sequence 1588, Ap
22	6	100.0	16	6	US-10-517-441-1798	Sequence 1798, Ap
23	6	100.0	16	6	US-10-517-441-1884	Sequence 1884, Ap
24	6	100.0	16	6	US-10-517-441-1924	Sequence 1924, Ap
25	6	100.0	16	6	US-10-539-953-5	Sequence 5, Appli
26	6	100.0	16	6	US-10-539-953-11	Sequence 11, Appl
27	6	100.0	16	6	US-10-539-953-13	Sequence 13, Appl
28	6	100.0	16	6	US-10-539-953-21	Sequence 21, Appl
29	6	100.0	16	6	US-10-539-953-26	Sequence 26, Appl
c 30	6	100.0	16	7	US-11-316-132-38	Sequence 38, Appl
c 31	6	100.0	17	6	US-10-514-776-55	Sequence 55, Appl
c 32	6	100.0	17	6	US-10-494-558B-21	Sequence 21, Appl
33	6	100.0	17	6	US-10-517-441-1634	Sequence 1634, Ap
34	6	100.0	17	6	US-10-517-441-1844	Sequence 1844, Ap
35	6	100.0	17	6	US-10-517-441-1922	Sequence 1922, Ap
36	6	100.0	17	6	US-10-517-441-2132	Sequence 2132, Ap
37	6	100.0	17	6	US-10-342-232-13	Sequence 13, Appl
38	6	100.0	17	6	US-10-524-432-437	Sequence 437, App
c 39	6	100.0	17	6	US-10-524-432-446	Sequence 446, App
40	6	100.0	17	6	US-10-524-432-502	Sequence 502, App
41	6	100.0	17	6	US-10-524-432-565	Sequence 565, App
42	6	100.0	17	6	US-10-524-432-662	Sequence 662, App
43	6	100.0	17	6	US-10-567-072-82	Sequence 82, Appl
44	6	100.0	17	6	US-10-567-072-83	Sequence 83, Appl
c 45	6	100.0	17	7	US-11-297-810-16	Sequence 16, Appl
c 46	6	100.0	18	6	US-10-501-834-72	Sequence 72, Appl
c 47	6	100.0	18	6	US-10-511-937-1932	Sequence 1932, Ap
c 48	6	100.0	18	6	US-10-511-937-2007	Sequence 2007, Ap
c 49	6	100.0	18	6	US-10-514-776-123	Sequence 123, App
c 50	6	100.0	18	6	US-10-514-776-227	Sequence 227, App
c 51	6	100.0	18	6	US-10-506-382-23	Sequence 23, Appl
c 52	6	100.0	18	6	US-10-517-441-218	Sequence 218, App
53	6	100.0	18	6	US-10-517-441-1284	Sequence 1284, Ap
54	6	100.0	18	6	US-10-517-441-1318	Sequence 1318, Ap
55	6	100.0	18	6	US-10-517-441-1350	Sequence 1350, Ap
56	6	100.0	18	6	US-10-517-441-1446	Sequence 1446, Ap
57	6	100.0	18	6	US-10-517-441-1479	Sequence 1479, Ap
58	6	100.0	18	6	US-10-517-441-1480	Sequence 1480, Ap
59	6	100.0	18	6	US-10-517-441-1724	Sequence 1724, Ap

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549977&ItemName=... 8/17/2006

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Score	Query	Match Length	DB	ID	Description
No.							
c	1	6	100.0	8	14	DU753265	DU753265 ASN3048.
	2	6	100.0	12	11	AQ074231	AQ074231 17 pUC8 P
c	3	6	100.0	12	11	BH169696	BH169696 SALK_0017
	4	6	100.0	12	14	AJ600541	AJ600541 Arabidops
	5	6	100.0	13	4	CA794347	CA794347 Cac_BL_13
	6	6	100.0	14	9	DR062980	DR062980 iq24c01.g
c	7	6	100.0	15	5	CF324040	CF324040 HDN--05-H
	8	6	100.0	15	7	AW248644	AW248644 2820747.3
	9	6	100.0	15	14	DU639534	DU639534 Ciuffi-HI
	10	6	100.0	16	14	AJ840730	AJ840730 Arabidops
	11	6	100.0	16	14	ATH525622	AJ525622 Arabidops
c	12	6	100.0	17	3	BQ589968	BQ589968 S013719-0
	13	6	100.0	18	3	BQ584794	BQ584794 E011673-0
	14	6	100.0	18	7	AW248796	AW248796 2820768.3
	15	6	100.0	19	1	AI149192	AI149192 qc76d09.x
c	16	6	100.0	19	1	AI251781	AI251781 qu76g01.x
c	17	6	100.0	19	1	AI443363	AI443363 sa31a08.x
c	18	6	100.0	19	1	AI624451	AI624451 ts29h11.x
c	19	6	100.0	19	1	AI635491	AI635491 ts65g09.x
c	20	6	100.0	19	1	AI641650	AI641650 fc22a01.x
c	21	6	100.0	19	1	AI719958	AI719958 as41d06.x
	22	6	100.0	19	4	CA794263	CA794263 Cac_BL_12
	23	6	100.0	19	5	CF325356	CF325356 JMT1--03-
c	24	6	100.0	19	5	CF848480	CF848480 psMA006xH
	25	6	100.0	19	7	AW248820	AW248820 2821008.3
c	26	6	100.0	19	7	AW250451	AW250451 2822502.3
	27	6	100.0	19	8	CV998328	CV998328 iv46f09.b
c	28	6	100.0	19	9	DR072936	DR072936 ik80a10.g
	29	6	100.0	19	11	AZ310299	AZ310299 1M0025011
	30	6	100.0	19	11	AZ316997	AZ316997 1M0035005
	31	6	100.0	19	11	AZ335137	AZ335137 1M0064P16
c	32	6	100.0	19	11	AZ344069	AZ344069 1M0077G21
	33	6	100.0	19	11	AZ358153	AZ358153 1M0100L23
	34	6	100.0	19	11	AZ412553	AZ412553 1M0186M03
	35	6	100.0	19	11	AZ422163	AZ422163 1M0200B22
c	36	6	100.0	19	11	AZ470171	AZ470171 1M0284C10
c	37	6	100.0	19	11	AZ474038	AZ474038 1M0290G15
	38	6	100.0	19	11	AZ493714	AZ493714 1M0328I04
	39	6	100.0	19	11	AZ493833	AZ493833 1M0328P11
	40	6	100.0	19	11	AZ579084	AZ579084 1M0363M07
	41	6	100.0	19	11	AZ634666	AZ634666 1M0490P03
	42	6	100.0	19	11	AZ645469	AZ645469 1M0510L24
	43	6	100.0	19	11	AZ771304	AZ771304 1M0573D22
	44	6	100.0	19	11	AZ777642	AZ777642 2M0012M20
	45	6	100.0	19	11	AZ781461	AZ781461 2M0019E20
	46	6	100.0	19	11	AZ840418	AZ840418 2M0136P21
c	47	6	100.0	20	1	AU257210	AU257210 AU257210
	48	6	100.0	20	5	CD533530	CD533530 32G11 Ara
	49	6	100.0	20	5	CF302797	CF302797 7LEAF--08
	50	6	100.0	20	9	DN988553	DN988553 ZEBRA_2F_
	51	6	100.0	20	11	AZ321845	AZ321845 1M0042A07
	52	6	100.0	20	11	AZ391065	AZ391065 1M0152H20
	53	6	100.0	20	11	AZ396417	AZ396417 1M0160P20

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-5.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-5.rge.

start

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

```
Run on:      June 29, 2006, 07:33:17 ; Search time 8113.04 Seconds
              (without alignments)
              9955.034 Million cell updates/sec
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Title:          US-10-615-005-5
Perfect score: 1263
Sequence:      1 atggcctcccgtaaacgcaa.....acttgggcagaggcagctga 1263
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1263	100.0	1263	2	AR264377	AR264377 Sequence
2	1263	100.0	1263	2	AR494852	AR494852 Sequence
3	1263	100.0	1263	2	AR779192	AR779192 Sequence
4	1263	100.0	12286	2	AR264383	AR264383 Sequence
5	1263	100.0	12286	2	AR494858	AR494858 Sequence
6	1263	100.0	12286	2	AR779198	AR779198 Sequence
7	1251.8	99.1	1362	2	AR264397	AR264397 Sequence
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9	1251.8	99.1	1362	2	AR779212	AR779212 Sequence
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11	1251.8	99.1	12571	2	AR494860	AR494860 Sequence
12	1251.8	99.1	12571	2	AR779200	AR779200 Sequence
13	1251.8	99.1	12886	4	AF186183	AF186183 Glycine m
14	1049.4	83.1	8573	4	AF186184	AF186184 Glycine m
15	649.4	51.4	9829	2	AR264384	AR264384 Sequence
16	649.4	51.4	9829	2	AR494859	AR494859 Sequence
17	649.4	51.4	9829	2	AR779199	AR779199 Sequence
18	649.4	51.4	10128	4	AF186182	AF186182 Glycine m
c 19	369.4	29.2	142370	12	AC166742	AC166742 Glycine m
c 20	340.4	27.0	173646	12	AC172299	AC172299 Glycine m
21	329	26.0	219053	12	AC167784	AC167784 Glycine m
22	324.2	25.7	175504	12	AC153161	AC153161 Glycine m
23	288.6	22.9	9139	2	AR264387	AR264387 Sequence
24	288.6	22.9	9139	2	AR494862	AR494862 Sequence
25	288.6	22.9	9139	2	AR779202	AR779202 Sequence
26	288.6	22.9	13637	4	AF186185	AF186185 Glycine m
27	255.4	20.2	186482	12	AC172298	AC172298 Glycine m
c 28	251	19.9	219053	12	AC167784	AC167784 Glycine m
29	115.6	9.2	4609	2	AR264386	AR264386 Sequence
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31	115.6	9.2	4609	2	AR779201	AR779201 Sequence
32	89.6	7.1	10482	2	AR264388	AR264388 Sequence
33	89.6	7.1	10482	2	AR494863	AR494863 Sequence
34	89.6	7.1	10482	2	AR779203	AR779203 Sequence
35	87.6	6.9	10510	4	AF186186	AF186186 Glycine m
c 36	70	5.5	175504	12	AC153161	AC153161 Glycine m
c 37	59	4.7	2000	2	AX655393	AX655393 Sequence
38	49.8	3.9	139267	4	AC144592	AC144592 Medicago
39	48.2	3.8	7218	2	I66494	I66494 Sequence 14
40	46.8	3.7	125020	5	AF429315	AF429315 Homo sapi
c 41	43.6	3.5	143285	5	AL139423	AL139423 Human DNA
42	42.8	3.4	2000	2	AX655393	AX655393 Sequence
c 43	42	3.3	110000	15	CP000143_16	Continuation (17 o
44	42	3.3	163144	12	AL365399	AL365399 Homo sapi
45	42	3.3	192628	6	AC160946	AC160946 Mus muscu

ALIGNMENTS

RESULT 1
AR264377

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549979&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1251.8	99.1	12571	3	AAZ35272	Aaz35272 Soybean r	
5	649.4	51.4	9829	3	AAZ35271	Aaz35271 Soybean r	
6	288.6	22.9	9139	3	AAZ35274	Aaz35274 Soybean r	
7	115.6	9.2	4609	3	AAZ35273	Aaz35273 Soybean r	
8	89.6	7.1	10482	3	AAZ35275	Aaz35275 Soybean r	
c 9	59	4.7	2000	8	ADA71938	Ada71938 Rice gene	
10	51.8	4.1	734	13	ADT17914	Adt17914 Plant cDN	
11	42.8	3.4	2000	8	ADA71938	Ada71938 Rice gene	
12	40.2	3.2	1254	3	AAZ35277	Aaz35277 Pea retro	
13	39.4	3.1	657	8	ABX17529	Abx17529 Human cDN	
14	39.4	3.1	727	5	AAH64747	Aah64747 Human sec	
15	39.4	3.1	1491	4	AAL05233	Aal05233 Human rep	
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19	39.4	3.1	1491	4	ABL98115	Ab198115 Human tes	
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21	39.4	3.1	2267	8	ABX17528	Abx17528 Human cDN	
22	38.6	3.1	1491	5	ADM19410	Adm19410 Novel hum	
23	38.2	3.0	1491	4	AAL01464	Aal01464 Human rep	
24	38.2	3.0	1491	4	ABL96910	Ab196910 Human tes	
25	38.2	3.0	1491	5	ADM19650	Adm19650 Novel hum	
26	37.4	3.0	4213	4	AAD06345	Aad06345 Sorghum d	
27	37.4	3.0	6827	4	AAD06344	Aad06344 Sorghum f	
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29	36.6	2.9	1743	3	AAZ86927	Aaz86927 Netrin co	
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31	36.6	2.9	4212	15	AEF63224	Aef63224 Mouse net	
c 32	36.2	2.9	23603	13	ABD33391	Abd33391 Murine ca	
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35	36	2.9	4454	4	AAK90985	Aak90985 Human dig	
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c 40	35.6	2.8	7918	2	AAX36583	Aax36583 BetaIII s	
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ALIGNMENTS

RESULT 1
AAZ35255

<http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549980&ItemName=...> 8/17/2006

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4	1263	100.0	12286	3	US-09-322-478-17	Sequence 17, Appl	
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6	1263	100.0	12286	3	US-10-799-870-17	Sequence 17, Appl	
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14	649.4	51.4	9829	3	US-09-586-106D-19	Sequence 19, Appl	
15	649.4	51.4	9829	3	US-10-799-870-19	Sequence 19, Appl	
16	288.6	22.9	9139	3	US-09-322-478-22	Sequence 22, Appl	
17	288.6	22.9	9139	3	US-09-586-106D-22	Sequence 22, Appl	
18	288.6	22.9	9139	3	US-10-799-870-22	Sequence 22, Appl	
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20	115.6	9.2	4609	3	US-09-586-106D-21	Sequence 21, Appl	
21	115.6	9.2	4609	3	US-10-799-870-21	Sequence 21, Appl	
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23	89.6	7.1	10482	3	US-09-586-106D-23	Sequence 23, Appl	
24	89.6	7.1	10482	3	US-10-799-870-23	Sequence 23, Appl	
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26	40.2	3.2	1254	3	US-09-322-478-25	Sequence 25, Appl	
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34	36.6	2.9	1743	3	US-08-482-677-9	Sequence 9, Appli	
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36	35.4	2.8	1086	3	US-08-914-372C-1	Sequence 1, Appli	
37	35.4	2.8	2230	4	US-10-094-749-1472	Sequence 1472, Ap	
38	35.4	2.8	109519	3	US-09-758-759-1	Sequence 1, Appli	
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ALIGNMENTS

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US-09-322-478-5

; Sequence 5, Application US/09322478

; Patent No. 6331662

; GENERAL INFORMATION:

; APPLICANT: Wright, David A.

; APPLICANT: Voytas, Daniel F.

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549981&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	1263	100.0	12286	8	US-10-615-005-17	Sequence 17, Appl
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	15	1251.8	99.1	12571	8	US-10-395-607-20	Sequence 20, Appl
	16	1251.8	99.1	12571	8	US-10-799-870-20	Sequence 20, Appl
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ALIGNMENTS

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c 17	33.8	2.7	889	7	US-11-266-748A-242170	Sequence 242170,
c 18	33.8	2.7	919	6	US-10-449-902-3213	Sequence 3213, Ap
c 19	33.8	2.7	940	6	US-10-449-902-14250	Sequence 14250, A
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c 42	33	2.6	5000	7	US-11-217-997-19	Sequence 19, Appl
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c 44	33	2.6	5005	7	US-11-217-997-21	Sequence 21, Appl
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ALIGNMENTS

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US-11-197-712-23

; Sequence 23, Application US/11197712

; Publication No. US20060130160A1

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Jobert, Severin

; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549983&ItemName=... 8/17/2006

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	16	262.8	20.8	406	13	CL878832	CL878832 abf27h03.
c	17	251	19.9	924	13	CZ501019	CZ501019 GMW2-27N3
	18	246.8	19.5	604	11	AZ221491	AZ221491 Gm_UMb001
c	19	241	19.1	412	13	CL880213	CL880213 abf43f05.
c	20	239.2	18.9	912	13	CZ505298	CZ505298 GMW2-19G5
c	21	234.2	18.5	912	13	CZ514763	CZ514763 GMW2-83A6
c	22	232.6	18.4	912	13	CZ499932	CZ499932 GMW2-17O2
c	23	231.4	18.3	930	13	CZ505975	CZ505975 GMW2-21J2
	24	231.4	18.3	935	13	CZ499877	CZ499877 GMW2-5L15
	25	228	18.1	905	12	CG824141	CG824141 SOYEU70TH
	26	226.4	17.9	927	13	CZ506659	CZ506659 GMW2-2P10
c	27	225.4	17.8	937	12	CG815341	CG815341 SOYEV14TH
	28	220.4	17.5	919	13	CZ501359	CZ501359 GMW2-9J1a
c	29	220.4	17.5	928	13	CZ515402	CZ515402 GMW2-84I1
	30	219.2	17.4	892	12	CG818454	CG818454 SOYFB78TV
	31	218.2	17.3	917	13	CZ514529	CZ514529 GMW2-40D1
	32	217.4	17.2	912	13	CZ522503	CZ522503 GMW2-82C1
c	33	214.2	17.0	918	12	CG824744	CG824744 SOYAC15TH
c	34	212.4	16.8	924	13	CZ527282	CZ527282 GMW2-143P
	35	211.2	16.7	486	13	CL885646	CL885646 abf73f09.
	36	211.2	16.7	950	13	CZ498565	CZ498565 GMW2-9E10
	37	207.4	16.4	433	13	CL888502	CL888502 abf91c09.
c	38	206.2	16.3	901	13	CL867806	CL867806 Gma_01_F1
	39	205.8	16.3	928	13	CZ519732	CZ519732 GMW2-61B1
	40	200.8	15.9	657	12	CG815752	CG815752 SOYFH77TV
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c	42	196.8	15.6	310	13	CL878833	CL878833 abf27h03.
c	43	196	15.5	773	12	CG813601	CG813601 SOYAJ37TH
c	44	196	15.5	856	12	CG821396	CG821396 SOYAN10TV
	45	195.4	15.5	493	13	CL900233	CL900233 abg58h01.

ALIGNMENTS

RESULT 1

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LOCUS CG818635 933 bp DNA linear GSS 18-NOV-2003

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549984&ItemName=... 8/17/2006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	603	100.0	12286	2	AR264383	AR264383 Sequence
5	603	100.0	12286	2	AR494858	AR494858 Sequence
6	603	100.0	12286	2	AR779198	AR779198 Sequence
7	566.2	93.9	603	2	AR264400	AR264400 Sequence
8	566.2	93.9	603	2	AR494875	AR494875 Sequence
9	566.2	93.9	603	2	AR779215	AR779215 Sequence
10	566.2	93.9	4609	2	AR264386	AR264386 Sequence
11	566.2	93.9	4609	2	AR494861	AR494861 Sequence
12	566.2	93.9	4609	2	AR779201	AR779201 Sequence
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14	542.4	90.0	12571	2	AR264385	AR264385 Sequence
15	542.4	90.0	12571	2	AR494860	AR494860 Sequence
16	542.4	90.0	12571	2	AR779200	AR779200 Sequence
17	542.4	90.0	12886	4	AF186183	AF186183 Glycine m
18	530.8	88.0	9829	2	AR264384	AR264384 Sequence
19	530.8	88.0	9829	2	AR494859	AR494859 Sequence
20	530.8	88.0	9829	2	AR779199	AR779199 Sequence
21	530.8	88.0	10128	4	AF186182	AF186182 Glycine m
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26	349.2	57.9	155108	12	AP007528	AP007528 Lotus cor
27	347.6	57.6	92281	4	AP004896	AP004896 Lotus cor
c 28	331.6	55.0	86045	12	AP007813	AP007813 Lotus cor
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34	323.8	53.7	87899	12	AC166090	AC166090 Glycine m
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43	306	50.7	79604	12	AC166911	AC166911 Glycine t
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ALIGNMENTS

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19	286.2	47.5	82138	3	AAF22305_10
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c 31	259.2	43.0	59590	3	AAF22281
32	251	41.6	628	10	ADC72532
33	245.8	40.8	699	10	ADC72415
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ALIGNMENTS

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ALIGNMENTS

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US-09-322-478-9

; Sequence 9, Application US/09322478

; Patent No. 6331662

; GENERAL INFORMATION:

; APPLICANT: Wright, David A.

; APPLICANT: Voytas, Daniel F.

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 9.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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40	289.4	48.0	64415	15	US-11-117-187-185	Sequence 185, App
41	289.4	48.0	94905	15	US-11-117-187-208	Sequence 208, App
c 42	289.4	48.0	1082144	15	US-11-117-187-211	Sequence 211, App
c 43	286.2	47.5	94905	15	US-11-117-187-208	Sequence 208, App
c 44	286.2	47.5	103931	15	US-11-117-187-193	Sequence 193, App
45	286.2	47.5	109974	15	US-11-117-187-204	Sequence 204, App

ALIGNMENTS

RESULT 1

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005- 9.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:36:14 ; Search time 1081 Seconds
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- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	603	100.0	603	3	US-09-965-553-9	Sequence 9, Appli
2	603	100.0	603	8	US-10-615-005-9	Sequence 9, Appli
3	603	100.0	603	8	US-10-395-607-9	Sequence 9, Appli
4	603	100.0	603	8	US-10-799-870-9	Sequence 9, Appli
5	603	100.0	12286	3	US-09-965-553-17	Sequence 17, Appl
6	603	100.0	12286	8	US-10-615-005-17	Sequence 17, Appl
7	603	100.0	12286	8	US-10-395-607-17	Sequence 17, Appl
8	603	100.0	12286	8	US-10-799-870-17	Sequence 17, Appl
9	566.2	93.9	603	3	US-09-965-553-35	Sequence 35, Appl
10	566.2	93.9	603	8	US-10-615-005-35	Sequence 35, Appl
11	566.2	93.9	603	8	US-10-395-607-35	Sequence 35, Appl
12	566.2	93.9	603	8	US-10-799-870-35	Sequence 35, Appl
13	566.2	93.9	4609	3	US-09-965-553-21	Sequence 21, Appl
14	566.2	93.9	4609	8	US-10-615-005-21	Sequence 21, Appl
15	566.2	93.9	4609	8	US-10-395-607-21	Sequence 21, Appl
16	566.2	93.9	4609	8	US-10-799-870-21	Sequence 21, Appl
17	542.4	90.0	12571	3	US-09-965-553-20	Sequence 20, Appl
18	542.4	90.0	12571	8	US-10-615-005-20	Sequence 20, Appl
19	542.4	90.0	12571	8	US-10-395-607-20	Sequence 20, Appl
20	542.4	90.0	12571	8	US-10-799-870-20	Sequence 20, Appl
21	530.8	88.0	9829	3	US-09-965-553-19	Sequence 19, Appl
22	530.8	88.0	9829	8	US-10-615-005-19	Sequence 19, Appl
23	530.8	88.0	9829	8	US-10-395-607-19	Sequence 19, Appl
24	530.8	88.0	9829	8	US-10-799-870-19	Sequence 19, Appl
25	360.4	59.8	10482	3	US-09-965-553-23	Sequence 23, Appl
26	360.4	59.8	10482	8	US-10-615-005-23	Sequence 23, Appl
27	360.4	59.8	10482	8	US-10-395-607-23	Sequence 23, Appl
28	360.4	59.8	10482	8	US-10-799-870-23	Sequence 23, Appl
29	327.2	54.3	9139	3	US-09-965-553-22	Sequence 22, Appl
30	327.2	54.3	9139	8	US-10-615-005-22	Sequence 22, Appl
31	327.2	54.3	9139	8	US-10-395-607-22	Sequence 22, Appl
32	327.2	54.3	9139	8	US-10-799-870-22	Sequence 22, Appl
33	308.6	51.2	13868	7	US-10-315-515-123	Sequence 123, App
34	305.4	50.6	13938	7	US-10-315-515-125	Sequence 125, App
35	305.4	50.6	13966	7	US-10-315-515-122	Sequence 122, App
36	305.4	50.6	14005	7	US-10-315-515-126	Sequence 126, App
37	303.8	50.4	14016	7	US-10-315-515-127	Sequence 127, App
38	295.8	49.1	79122	15	US-11-117-187-200	Sequence 200, App
39	291	48.3	129021	15	US-11-117-187-202	Sequence 202, App
40	289.4	48.0	64415	15	US-11-117-187-185	Sequence 185, App
41	289.4	48.0	94905	15	US-11-117-187-208	Sequence 208, App
c 42	289.4	48.0	1082144	15	US-11-117-187-211	Sequence 211, App
c 43	286.2	47.5	94905	15	US-11-117-187-208	Sequence 208, App
c 44	286.2	47.5	103931	15	US-11-117-187-193	Sequence 193, App
45	286.2	47.5	109974	15	US-11-117-187-204	Sequence 204, App

ALIGNMENTS

RESULT 1

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-9.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-9.rnpbn.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 08:51:49 ; Search time 90.7449 Seconds
(without alignments)
7857.686 Million cell updates/sec

Title: US-10-615-005-9
Perfect score: 603
Sequence: 1 tgtgataaatgccagagAAC.....tcaagttgctcaactttgac 603

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	96	15.9	3732	6	US-10-449-902-12764	Sequence 12764, A
2	61.8	10.2	3187	6	US-10-449-902-9357	Sequence 9357, Ap
3	55.2	9.2	2027	6	US-10-449-902-6874	Sequence 6874, Ap
c 4	52.6	8.7	1876	6	US-10-953-349-38211	Sequence 38211, A
5	52.2	8.7	2360	6	US-10-449-902-25434	Sequence 25434, A
6	52	8.6	1738	6	US-10-449-902-7359	Sequence 7359, Ap
7	47.8	7.9	1438	6	US-10-449-902-2898	Sequence 2898, Ap
8	46.4	7.7	1237661	7	US-11-266-748A-29041	Sequence 29041, A
9	45.8	7.6	2521	7	US-11-293-697-427	Sequence 427, App
10	45.4	7.5	1598	6	US-10-449-902-1567	Sequence 1567, Ap
11	45.4	7.5	4559	6	US-10-449-902-17469	Sequence 17469, A
12	45.4	7.5	5050	6	US-10-449-902-28374	Sequence 28374, A
c 13	45.2	7.5	612	7	US-11-266-748A-254198	Sequence 254198,
14	45.2	7.5	612	7	US-11-266-748A-314715	Sequence 314715,
15	45.2	7.5	8764	7	US-11-322-999-137	Sequence 137, App
16	45.2	7.5	8916	7	US-11-322-999-139	Sequence 139, App
17	43.8	7.3	4545	7	US-11-238-031-113	Sequence 113, App
18	43.8	7.3	6140	7	US-11-238-031-21	Sequence 21, Appl
19	43.6	7.2	8919	7	US-11-322-999-138	Sequence 138, App
20	43.2	7.2	1288	6	US-10-449-902-4818	Sequence 4818, Ap
21	43.2	7.2	38542	7	US-11-266-748A-28984	Sequence 28984, A
22	42.8	7.1	4187	6	US-10-449-902-18580	Sequence 18580, A
c 23	42.6	7.1	1000	7	US-11-266-748A-199133	Sequence 199133,
c 24	41.4	6.9	873	7	US-11-266-748A-17739	Sequence 17739, A
25	41.4	6.9	2688	7	US-11-293-697-364	Sequence 364, App
26	40.4	6.7	1000	7	US-11-266-748A-282295	Sequence 282295,
c 27	40.4	6.7	1000	7	US-11-266-748A-308935	Sequence 308935,
28	38	6.3	4498	7	US-11-217-529-190990	Sequence 190990,
29	37	6.1	1883	6	US-10-449-902-7465	Sequence 7465, Ap
30	36.8	6.1	613	6	US-10-449-902-5507	Sequence 5507, Ap
31	36.6	6.1	713	6	US-10-953-349-40209	Sequence 40209, A
32	36.6	6.1	126259	7	US-11-266-748A-61158	Sequence 61158, A
33	36.2	6.0	2298	7	US-11-217-529-1611	Sequence 1611, Ap
34	35.2	5.8	1000	7	US-11-266-748A-220733	Sequence 220733,
c 35	35.2	5.8	1000	7	US-11-266-748A-246399	Sequence 246399,
36	35.2	5.8	1000	7	US-11-266-748A-284300	Sequence 284300,
c 37	35.2	5.8	1000	7	US-11-266-748A-335729	Sequence 335729,
38	35.2	5.8	1000	7	US-11-266-748A-394262	Sequence 394262,
c 39	35.2	5.8	1000	7	US-11-266-748A-465308	Sequence 465308,
40	34.6	5.7	56093	7	US-11-266-748A-61305	Sequence 61305, A
41	34.2	5.7	6407	7	US-11-266-748A-28275	Sequence 28275, A
c 42	34	5.6	142599	7	US-11-266-748A-59766	Sequence 59766, A
c 43	33.8	5.6	1000	7	US-11-266-748A-196688	Sequence 196688,
44	33.8	5.6	2833	6	US-10-449-902-9264	Sequence 9264, Ap
c 45	33.6	5.6	1409	7	US-11-266-748A-186416	Sequence 186416,

ALIGNMENTS

RESULT 1

US-10-449-902-12764

; Sequence 12764, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

<http://es.ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=549989&ItemName=...> 8/17/2006

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
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1	463.2	76.8	930	13	CZ501630
2	449.2	74.5	924	13	CZ514008
3	398	66.0	472	13	CL882911
c 4	396.6	65.8	484	13	CL887535
5	391	64.8	476	13	CL889972
c 6	336.6	55.8	929	13	CZ512993
c 7	331.6	55.0	914	13	CZ510745
8	329.4	54.6	1011	11	BH675008
c 9	328.4	54.5	915	13	CZ527232
c 10	328.2	54.4	815	13	CL867447
11	327.8	54.4	688	11	BH528843
12	327.8	54.4	773	11	BH468408
c 13	326.8	54.2	914	13	CZ527022
c 14	326.8	54.2	919	13	CZ518743
15	326.2	54.1	739	11	BH592174
16	326.2	54.1	820	11	BZ505678
c 17	323.6	53.7	919	13	CZ527246
18	323	53.6	775	11	BH450168
19	321.4	53.3	767	14	DX044376
20	321.2	53.3	725	11	BH974426
21	319.8	53.0	748	11	BH673125
22	318.2	52.8	855	14	DX060785
23	318.2	52.8	865	14	DX075483
c 24	317.4	52.6	923	12	CG818428
25	316.6	52.5	769	14	DX064309
26	316.6	52.5	813	14	DX055939
c 27	316.6	52.5	821	14	CT022195
28	316.6	52.5	851	14	DX032482
29	315.6	52.3	727	14	DX034149
c 30	315	52.2	696	11	BH928310
31	315	52.2	741	14	DX017925
32	315	52.2	764	11	BH454730
33	315	52.2	777	14	DX061248
34	315	52.2	806	14	DX052948
35	315	52.2	818	14	DX051410
c 36	314.4	52.1	929	13	CZ504422
37	313.4	52.0	646	11	BZ515239
c 38	310.4	51.5	483	13	CL884361
39	310.2	51.4	817	14	DX015902
c 40	309.6	51.3	782	11	BH489791
41	308.6	51.2	732	11	BZ478737
c 42	307.6	51.0	795	11	BH522839
43	307.2	50.9	698	14	DX021885
44	307	50.9	695	11	BH499049
45	307	50.9	719	11	BH421567

ALIGNMENTS

RESULT 1

CZ501630

LOCUS CZ501630 930 bp DNA linear GSS 11-MAY-2005

http://es/ScoreAccessWeb/GetItem.action?AppId=10615005&seqId=548900&ItemName=... 8/17/2006

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	7	3	AAY32476	Aay32476 Retroelem
2	33	100.0	59	7	ADJ81444	Adj81444 Plant ret
3	33	100.0	420	3	AAY32428	Aay32428 Plant ret
4	30	90.9	59	7	ADJ81441	Adj81441 Plant ret
5	30	90.9	65	8	ADR94514	Adr94514 Novel S.
6	30	90.9	65	9	AEA58384	Aea58384 Streptoco
7	30	90.9	312	2	AAR97843	Aar97843 Kaposi's
8	30	90.9	312	2	AAR93605	Aar93605 Kaposi's
9	29	87.9	22	9	ADV52562	Adv52562 Gamma-sec
10	29	87.9	23	9	ADV52561	Adv52561 Gamma-sec
11	29	87.9	30	9	ADV52560	Adv52560 Gamma-sec
12	29	87.9	31	9	ADV52559	Adv52559 Gamma-sec
13	29	87.9	44	5	ABB53147	Abb53147 Human ORF
14	29	87.9	125	5	ABP04833	Abp04833 Human ORF
15	29	87.9	129	5	ADK36584	Adk36584 Novel hum
16	29	87.9	204	4	ABG20952	Abg20952 Novel hum
17	29	87.9	217	8	ADT58036	Adt58036 Plant pol
18	29	87.9	241	8	ADT57076	Adt57076 Plant pol
19	29	87.9	773	4	AAB93701	Aab93701 Human pro
20	29	87.9	773	6	ABR39451	Abr39451 Notch-int
21	29	87.9	781	8	ADN60395	Adn60395 B. lichen
22	29	87.9	781	8	ADN60505	Adn60505 B. lichen
23	29	87.9	781	8	ADN60519	Adn60519 B. lichen
24	29	87.9	1015	9	AEB55332	Aeb55332 Human not
25	29	87.9	2000	8	ADP25398	Adp25398 PRO polyp
26	29	87.9	2109	9	ADZ13391	Adz13391 Human can
27	29	87.9	2109	9	ADZ13393	Adz13393 Human can
28	29	87.9	2225	8	ABO85005	Abo85005 Human can
29	29	87.9	2469	5	AAE18207	Aae18207 Human MOL
30	29	87.9	2469	7	ADD18192	Add18192 Human mol
31	29	87.9	2471	2	AAO27065	Aao27065 Human Not
32	29	87.9	2471	2	AAY06816	Aay06816 Human Not
33	29	87.9	2471	6	AAG79774	Aag79774 Human Not
34	29	87.9	2471	6	ABP72572	Abp72572 Human Not
35	29	87.9	2471	6	ABR61831	Abr61831 Human Not
36	29	87.9	2471	7	ABR61760	Abr61760 Human Not
37	29	87.9	2471	7	ADE58245	Ade58245 Human Pro
38	29	87.9	2471	7	ADE63707	Ade63707 Human Pro
39	29	87.9	2471	7	ADE63703	Ade63703 Human Pro
40	29	87.9	2471	7	ADE63715	Ade63715 Human Pro
41	29	87.9	2471	7	ADE58243	Ade58243 Rat Prote
42	29	87.9	2471	7	ADE63711	Ade63711 Human Pro
43	29	87.9	2471	8	ADL26913	Adl26913 Human Not
44	29	87.9	2471	8	ADM41517	Adm41517 Human Not
45	29	87.9	2471	8	ADN30468	Adn30468 Human Not
46	29	87.9	2471	8	ADP67249	Adp67249 Human Not
47	29	87.9	2471	9	ADX70403	Adx70403 Human Not
48	29	87.9	2471	9	AEA08677	Aea08677 Human Not
49	29	87.9	2471	9	AED15428	Aed15428 Equine Pr
50	29	87.9	2471	9	AED08742	Aed08742 Human Not
51	29	87.9	2471	10	AEF79174	Aef79174 Human NOT
52	29	87.9	2473	9	ADZ13388	Adz13388 Murine ca
53	29	87.9	2527	8	ABO85004	Abo85004 Murine ca
54	28	84.8	8	8	ADK10820	Adk10820 Human pap
55	28	84.8	10	8	ADK10828	Adk10828 Human pap
56	28	84.8	59	3	AAB42694	Aab42694 Human ORF
57	28	84.8	60	5	ABP34014	Abp34014 Human ORF

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-4

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-4.rai.

[start](#)

[Go Back to p](#)

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OM protein - protein search, using sw model

Run on: June 28, 2006, 15:37:46 ; Search time 50 Seconds
(without alignments)
12.254 Million cell updates/sec

Title: US-10-615-005-4
Perfect score: 33
Sequence: 1 MASRKRK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	33	100.0	7	2	US-09-322-478-4 Sequence 4, Appli
2	33	100.0	7	2	US-09-586-106D-4 Sequence 4, Appli

3	33	100.0	7	2	US-10-799-870-4	Sequence 4, Appli
4	33	100.0	421	2	US-09-322-478-6	Sequence 6, Appli
5	33	100.0	421	2	US-09-586-106D-6	Sequence 6, Appli
6	33	100.0	421	2	US-10-799-870-6	Sequence 6, Appli
7	30	90.9	65	2	US-09-107-433-3149	Sequence 3149, Ap
8	30	90.9	80	2	US-09-248-796A-21674	Sequence 21674, A
9	30	90.9	312	1	US-08-420-235B-11	Sequence 11, Appl
10	30	90.9	312	2	US-08-793-624-11	Sequence 11, Appl
11	30	90.9	312	5	PCT-US95-10194-11	Sequence 11, Appl
12	29	87.9	136	2	US-09-248-796A-27752	Sequence 27752, A
13	29	87.9	1015	1	US-08-537-210A-1	Sequence 1, Appli
14	29	87.9	1015	2	US-09-113-825-1	Sequence 1, Appli
15	29	87.9	2471	1	US-08-185-432-16	Sequence 16, Appl
16	29	87.9	2471	1	US-08-083-590A-19	Sequence 19, Appl
17	29	87.9	2471	2	US-08-532-384-19	Sequence 19, Appl
18	29	87.9	2471	2	US-08-899-232-1	Sequence 1, Appli
19	29	87.9	2471	2	US-09-121-457-1	Sequence 1, Appli
20	28	84.8	388	2	US-09-489-039A-11478	Sequence 11478, A
21	28	84.8	437	2	US-09-107-532A-6421	Sequence 6421, Ap
22	28	84.8	500	2	US-09-107-532A-4085	Sequence 4085, Ap
23	28	84.8	519	2	US-10-113-794A-2	Sequence 2, Appli
24	28	84.8	520	2	US-09-949-016-9918	Sequence 9918, Ap
25	28	84.8	548	2	US-09-252-991A-27696	Sequence 27696, A
26	28	84.8	923	3	US-10-114-270-152	Sequence 152, App
27	28	84.8	930	2	US-10-113-794A-1	Sequence 1, Appli
28	27	81.8	66	2	US-09-248-796A-23472	Sequence 23472, A
29	27	81.8	76	2	US-09-513-999C-6143	Sequence 6143, Ap
30	27	81.8	126	2	US-09-710-279-2094	Sequence 2094, Ap
31	27	81.8	153	2	US-09-270-767-34465	Sequence 34465, A
32	27	81.8	153	2	US-09-270-767-49682	Sequence 49682, A
33	27	81.8	158	2	US-09-949-016-10052	Sequence 10052, A
34	27	81.8	175	2	US-09-605-703B-2624	Sequence 2624, Ap
35	27	81.8	222	7	5386025-2	Patent No. 5386025
36	27	81.8	242	2	US-08-977-865-4	Sequence 4, Appli
37	27	81.8	310	2	US-09-907-794A-153	Sequence 153, App
38	27	81.8	310	2	US-09-905-125A-153	Sequence 153, App
39	27	81.8	310	2	US-09-902-775A-153	Sequence 153, App
40	27	81.8	310	2	US-09-906-700-153	Sequence 153, App
41	27	81.8	310	2	US-09-903-603A-153	Sequence 153, App
42	27	81.8	310	2	US-09-904-920A-153	Sequence 153, App
43	27	81.8	310	2	US-09-909-064-153	Sequence 153, App
44	27	81.8	310	2	US-09-905-381A-153	Sequence 153, App
45	27	81.8	310	2	US-09-906-618-153	Sequence 153, App
46	27	81.8	310	2	US-09-906-646-153	Sequence 153, App
47	27	81.8	310	2	US-09-904-462-153	Sequence 153, App
48	27	81.8	310	2	US-09-902-736A-153	Sequence 153, App
49	27	81.8	310	2	US-09-906-722A-153	Sequence 153, App
50	27	81.8	310	2	US-09-905-449-153	Sequence 153, App
51	27	81.8	310	2	US-09-903-562B-153	Sequence 153, App
52	27	81.8	310	2	US-09-906-679A-153	Sequence 153, App
53	27	81.8	310	3	US-09-907-841-153	Sequence 153, App
54	27	81.8	325	2	US-09-311-021-74	Sequence 74, Appl
55	27	81.8	325	2	US-09-806-536A-10	Sequence 10, Appl
56	27	81.8	352	2	US-09-576-160B-3	Sequence 3, Appli
57	27	81.8	390	2	US-08-977-865-2	Sequence 2, Appli
58	27	81.8	442	2	US-09-032-365A-17	Sequence 17, Appl
59	27	81.8	456	2	US-09-949-016-8968	Sequence 8968, Ap
60	27	81.8	462	2	US-09-252-991A-21704	Sequence 21704, A
61	27	81.8	491	2	US-08-812-824-1	Sequence 1, Appli
62	27	81.8	676	2	US-09-939-853A-41	Sequence 41, Appl
63	27	81.8	927	2	US-09-252-991A-31823	Sequence 31823, A

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-4.rapbm

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This page gives you Search Results detail for the Application 10615005 and Search Result us-10-615-005-4.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 15:38:00 ; Search time 185 Seconds
(without alignments)
17.527 Million cell updates/sec

Title: US-10-615-005-4
Perfect score: 33
Sequence: 1 MASRKRK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	33	100.0	7	3	US-09-965-553-4	Sequence 4, Appli
2	33	100.0	7	4	US-10-615-005-4	Sequence 4, Appli
3	33	100.0	7	4	US-10-395-607-4	Sequence 4, Appli

4	33	100.0	7	4	US-10-799-870-4	Sequence 4, Appli
5	33	100.0	24	4	US-10-315-515-57	Sequence 57, Appl
6	33	100.0	104	4	US-10-424-599-165308	Sequence 165308,
7	33	100.0	216	4	US-10-424-599-199938	Sequence 199938,
8	33	100.0	395	4	US-10-424-599-258900	Sequence 258900,
9	33	100.0	421	3	US-09-965-553-6	Sequence 6, Appli
10	33	100.0	421	4	US-10-615-005-6	Sequence 6, Appli
11	33	100.0	421	4	US-10-395-607-6	Sequence 6, Appli
12	33	100.0	421	4	US-10-799-870-6	Sequence 6, Appli
13	30	90.9	24	4	US-10-315-515-53	Sequence 53, Appl
14	30	90.9	63	4	US-10-437-963-169816	Sequence 169816,
15	30	90.9	65	5	US-10-617-320-3149	Sequence 3149, Ap
16	30	90.9	116	4	US-10-767-701-36506	Sequence 36506, A
17	30	90.9	123	4	US-10-425-115-300420	Sequence 300420,
18	30	90.9	703	6	US-11-079-463-8735	Sequence 8735, Ap
19	29	87.9	44	3	US-09-826-734-240	Sequence 240, App
20	29	87.9	109	4	US-10-424-599-178966	Sequence 178966,
21	29	87.9	116	4	US-10-424-599-237812	Sequence 237812,
22	29	87.9	196	4	US-10-437-963-115251	Sequence 115251,
23	29	87.9	204	5	US-10-450-763-51311	Sequence 51311, A
24	29	87.9	217	5	US-10-739-930-8113	Sequence 8113, Ap
25	29	87.9	220	4	US-10-425-115-225420	Sequence 225420,
26	29	87.9	241	5	US-10-739-930-7153	Sequence 7153, Ap
27	29	87.9	242	4	US-10-425-115-225422	Sequence 225422,
28	29	87.9	773	4	US-10-225-630-6	Sequence 6, Appli
29	29	87.9	773	6	US-11-133-849-6	Sequence 6, Appli
30	29	87.9	781	5	US-10-510-408-67	Sequence 67, Appl
31	29	87.9	781	5	US-10-510-408-177	Sequence 177, App
32	29	87.9	781	5	US-10-510-408-191	Sequence 191, App
33	29	87.9	1015	4	US-10-419-026-1	Sequence 1, Appli
34	29	87.9	1015	5	US-10-746-237-1	Sequence 1, Appli
35	29	87.9	2203	4	US-10-322-281-726	Sequence 726, App
36	29	87.9	2469	4	US-10-190-115-2	Sequence 2, Appli
37	29	87.9	2469	4	US-10-369-072-2	Sequence 2, Appli
38	29	87.9	2471	4	US-10-190-115-27	Sequence 27, Appl
39	29	87.9	2471	4	US-10-369-072-27	Sequence 27, Appl
40	29	87.9	2471	4	US-10-720-896A-12	Sequence 12, Appl
41	29	87.9	2471	5	US-10-765-727-23	Sequence 23, Appl
42	29	87.9	2471	5	US-10-846-989-57	Sequence 57, Appl
43	29	87.9	2471	5	US-10-764-415B-40	Sequence 40, Appl
44	29	87.9	2471	5	US-10-781-060-19	Sequence 19, Appl
45	29	87.9	2471	5	US-10-845-834A-57	Sequence 57, Appl
46	29	87.9	2471	6	US-11-050-346-68	Sequence 68, Appl
47	29	87.9	2503	4	US-10-322-281-723	Sequence 723, App
48	28	84.8	60	3	US-09-864-408A-5974	Sequence 5974, Ap
49	28	84.8	67	3	US-09-864-408A-3480	Sequence 3480, Ap
50	28	84.8	95	4	US-10-425-115-291928	Sequence 291928,
51	28	84.8	109	6	US-11-096-568A-19969	Sequence 19969, A
52	28	84.8	110	6	US-11-096-568A-19968	Sequence 19968, A
53	28	84.8	161	4	US-10-767-701-37441	Sequence 37441, A
54	28	84.8	161	4	US-10-425-115-291929	Sequence 291929,
55	28	84.8	161	6	US-11-096-568A-19967	Sequence 19967, A
56	28	84.8	162	4	US-10-425-115-291927	Sequence 291927,
57	28	84.8	184	5	US-10-490-147A-12	Sequence 12, Appl
58	28	84.8	189	5	US-10-467-657-4524	Sequence 4524, Ap
59	28	84.8	192	5	US-10-739-930-10277	Sequence 10277, A
60	28	84.8	304	4	US-10-072-012-727	Sequence 727, App
61	28	84.8	317	5	US-10-739-930-8074	Sequence 8074, Ap
62	28	84.8	430	4	US-10-282-122A-57774	Sequence 57774, A
63	28	84.8	446	6	US-11-096-568A-27614	Sequence 27614, A
64	28	84.8	448	4	US-10-437-963-201571	Sequence 201571,

SCORE Search Results Details for Application 10615005 and Search Result us-10-615-005-4.rapbn.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 15:39:10 ; Search time 20 Seconds
(without alignments)
8.267 Million cell updates/sec

Title: US-10-615-005-4
Perfect score: 33
Sequence: 1 MASRKRK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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1	29	87.9	196	6	US-10-449-902-30713	Sequence 30713, A
2	29	87.9	210	6	US-10-449-902-40915	Sequence 40915, A
3	29	87.9	943	6	US-10-449-902-41329	Sequence 41329, A
4	28	84.8	134	6	US-10-953-349-15115	Sequence 15115, A
5	28	84.8	164	6	US-10-953-349-29314	Sequence 29314, A
6	28	84.8	165	6	US-10-953-349-15114	Sequence 15114, A
7	28	84.8	200	6	US-10-953-349-29313	Sequence 29313, A
8	28	84.8	467	6	US-10-449-902-43743	Sequence 43743, A
9	28	84.8	591	7	US-11-293-697-3970	Sequence 3970, Ap
10	27	81.8	120	6	US-10-449-902-45630	Sequence 45630, A
11	27	81.8	123	6	US-10-953-349-33117	Sequence 33117, A
12	27	81.8	155	6	US-10-953-349-33115	Sequence 33115, A
13	27	81.8	169	6	US-10-449-902-39309	Sequence 39309, A
14	27	81.8	1596	6	US-10-449-902-41069	Sequence 41069, A
15	26	78.8	135	6	US-10-953-349-35020	Sequence 35020, A
16	26	78.8	163	6	US-10-953-349-35019	Sequence 35019, A
17	26	78.8	163	6	US-10-449-902-51629	Sequence 51629, A
18	26	78.8	177	6	US-10-953-349-12972	Sequence 12972, A
19	26	78.8	225	6	US-10-953-349-35018	Sequence 35018, A
20	26	78.8	244	7	US-11-197-712-359	Sequence 359, App
21	26	78.8	246	6	US-10-953-349-12971	Sequence 12971, A
22	26	78.8	249	6	US-10-449-902-40085	Sequence 40085, A
23	26	78.8	271	6	US-10-953-349-12970	Sequence 12970, A
24	26	78.8	313	6	US-10-953-349-17837	Sequence 17837, A
25	26	78.8	331	6	US-10-953-349-17836	Sequence 17836, A
26	26	78.8	370	6	US-10-953-349-17835	Sequence 17835, A
27	26	78.8	460	6	US-10-449-902-43231	Sequence 43231, A
28	26	78.8	636	6	US-10-449-902-44935	Sequence 44935, A
29	26	78.8	730	6	US-10-449-902-51873	Sequence 51873, A
30	26	78.8	1003	6	US-10-449-902-56511	Sequence 56511, A
31	26	78.8	1095	6	US-10-449-902-41211	Sequence 41211, A
32	26	78.8	1207	7	US-11-273-537-25	Sequence 25, Appl
33	25	75.8	67	6	US-10-471-571A-454	Sequence 454, App
34	25	75.8	101	6	US-10-953-349-38431	Sequence 38431, A
35	25	75.8	121	6	US-10-449-902-38267	Sequence 38267, A
36	25	75.8	142	6	US-10-953-349-10259	Sequence 10259, A
37	25	75.8	152	6	US-10-953-349-10258	Sequence 10258, A
38	25	75.8	153	6	US-10-449-902-32194	Sequence 32194, A
39	25	75.8	160	6	US-10-449-902-30264	Sequence 30264, A
40	25	75.8	160	6	US-10-449-902-32348	Sequence 32348, A
41	25	75.8	174	6	US-10-953-349-10257	Sequence 10257, A
42	25	75.8	206	6	US-10-953-349-1325	Sequence 1325, Ap
43	25	75.8	207	6	US-10-449-902-30471	Sequence 30471, A
44	25	75.8	207	6	US-10-449-902-48374	Sequence 48374, A
45	25	75.8	214	6	US-10-449-902-39298	Sequence 39298, A
46	25	75.8	240	6	US-10-953-349-1324	Sequence 1324, Ap
47	25	75.8	257	6	US-10-449-902-40769	Sequence 40769, A
48	25	75.8	275	6	US-10-449-902-47010	Sequence 47010, A
49	25	75.8	277	6	US-10-449-902-54695	Sequence 54695, A
50	25	75.8	283	6	US-10-449-902-32047	Sequence 32047, A
51	25	75.8	283	6	US-10-449-902-56219	Sequence 56219, A
52	25	75.8	298	6	US-10-449-902-37390	Sequence 37390, A
53	25	75.8	298	6	US-10-449-902-37474	Sequence 37474, A
54	25	75.8	298	6	US-10-449-902-39708	Sequence 39708, A
55	25	75.8	301	6	US-10-953-349-3943	Sequence 3943, Ap
56	25	75.8	303	6	US-10-449-902-50401	Sequence 50401, A
57	25	75.8	331	6	US-10-953-349-3684	Sequence 3684, Ap
58	25	75.8	351	6	US-10-505-928-712	Sequence 712, App
59	25	75.8	358	6	US-10-953-349-4979	Sequence 4979, Ap

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This page gives you Search Results detail for the Application 10615005 and Search Result us-10-6:
start

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OM protein - protein search, using sw model

Run on: June 28, 2006, 15:32:45 ; Search time 39 Seconds
(without alignments)
17.270 Million cell updates/sec

Title: US-10-615-005-4
Perfect score: 33
Sequence: 1 MASRKRK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	30	90.9	207	2	T12579	GTP-binding protei
2	30	90.9	226	2	I49392	gene xlr3b protein
3	29	87.9	280	2	T32325	hypothetical prote
4	29	87.9	892	2	T27005	hypothetical prote
5	29	87.9	2471	2	A49128	cell-fate determin
6	28	84.8	306	2	E97471	hypothetical prote
7	28	84.8	465	2	E96737	probable DEAD/DEAH
8	28	84.8	519	2	S78089	G-protein signalin

9	28	84.8	533	2	T06153	hypothetical prote
10	28	84.8	547	2	S41618	probable DNA-direc
11	28	84.8	919	1	PXZP1P	H+-exporting ATPas
12	28	84.8	935	2	S62476	hypothetical prote
13	28	84.8	1128	1	DNBEM1	DNA-binding protei
14	28	84.8	1244	2	T19068	hypothetical prote
15	28	84.8	1944	2	A59438	KIAA1424 protein [
16	27	81.8	44	2	AG1431	ribosomal protein
17	27	81.8	44	2	AE1805	ribosomal protein
18	27	81.8	65	2	S52345	hypothetical prote
19	27	81.8	126	2	H86347	hypothetical prote
20	27	81.8	169	2	H81071	conserved hypothet
21	27	81.8	173	2	I54328	myosin regulatory
22	27	81.8	173	2	JC2242	superfast myosin 1
23	27	81.8	184	2	T24251	hypothetical prote
24	27	81.8	315	2	T15165	hypothetical prote
25	27	81.8	325	2	T17307	hypothetical prote
26	27	81.8	374	2	B83241	conserved hypothet
27	27	81.8	399	2	A97526	hypothetical prote
28	27	81.8	399	2	AB2745	conserved hypothet
29	27	81.8	421	2	T38242	probable phosphata
30	27	81.8	425	2	T20691	hypothetical prote
31	27	81.8	616	2	C83404	conserved hypothet
32	27	81.8	768	2	A29066	DNA ligase (ATP) (
33	27	81.8	830	2	A34347	translation elonga
34	27	81.8	1034	2	S49947	SMT4 protein - yea
35	26	78.8	23	2	PH0858	MauD protein - Par
36	26	78.8	65	2	I40892	hypothetical prote
37	26	78.8	89	1	H64116	ribosomal protein
38	26	78.8	95	1	A69697	ribosomal protein
39	26	78.8	164	1	D69783	transcription regu
40	26	78.8	178	2	C64168	hypothetical prote
41	26	78.8	204	2	T23043	hypothetical prote
42	26	78.8	216	2	T50314	probable human pop
43	26	78.8	226	2	I48880	X-linked lymphocyt
44	26	78.8	243	2	T08785	hypothetical prote
45	26	78.8	271	2	S42728	phosphodiesterase
46	26	78.8	348	2	T21648	hypothetical prote
47	26	78.8	362	2	S01091	fodrin alpha chain
48	26	78.8	378	2	E84806	probable elongatio
49	26	78.8	386	2	S54153	serotonin receptor
50	26	78.8	386	2	A42688	serotonin receptor
51	26	78.8	386	2	S18637	serotonin receptor
52	26	78.8	389	2	S68422	serotonin receptor
53	26	78.8	390	2	JN0268	serotonin receptor
54	26	78.8	390	2	S58126	serotonin receptor
55	26	78.8	395	2	AD3354	hypothetical cytos
56	26	78.8	397	2	F90449	conserved hypothet
57	26	78.8	434	2	S37907	hypothetical prote
58	26	78.8	457	2	T33820	hypothetical prote
59	26	78.8	458	2	T26630	hypothetical prote
60	26	78.8	462	2	T32751	hypothetical prote
61	26	78.8	462	2	T19830	hypothetical prote
62	26	78.8	478	2	C29514	muscarinic acetylch
63	26	78.8	479	2	S10127	muscarinic acetylch
64	26	78.8	479	2	S33776	muscarinic acetylch
65	26	78.8	480	2	D75053	hypothetical prote
66	26	78.8	490	2	S28355	hypothetical prote
67	26	78.8	505	2	S68518	tub protein, brain
68	26	78.8	509	2	T01344	hypothetical prote
69	26	78.8	572	1	FOHYIH	retrovirus-related

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5	30	90.9	226	1	XL3B_MOUSE	Q61806	mus musculu
6	30	90.9	226	2	Q6P205_MOUSE	Q6p205	mus musculu
7	30	90.9	275	2	Q8EX41_MYCPE	Q8ex41	mycoplasma
8	30	90.9	277	2	Q7NX15_CHRVO	Q7nx15	chromobacte
9	30	90.9	312	2	Q98133_HHV8	Q98133	human herpe
10	30	90.9	334	2	O40929_HHV8	O40929	human herpe
11	30	90.9	374	2	Q4ITV5_AZOVI	Q4itv5	azotobacter
12	30	90.9	374	2	Q3KGD8_PSEPF	Q3kgd8	pseudomonas
13	30	90.9	383	2	Q2SQ08_9GAMM	Q2sq08	hahella che
14	30	90.9	393	2	Q5FSB9_GLUOX	Q5fsb9	gluconobact
15	30	90.9	395	2	Q92Q59_RHIME	Q92q59	rhizobium m
16	30	90.9	396	2	Q2K8Z1_RHIET	Q2k8z1	rhizobium e
17	30	90.9	397	2	Q3WRM9_9RHIZ	Q3wrm9	mesorhizobi
18	30	90.9	404	2	Q98MA6_RHILO	Q98ma6	rhizobium l
19	30	90.9	432	2	Q53IM5_FUGRU	Q53im5	fugu rubrip
20	30	90.9	465	2	Q9QP16_9ALPH	Q9qp16	gallid herp
21	30	90.9	534	2	Q4P3G4_USTMA	Q4p3g4	ustilago ma
22	30	90.9	569	2	Q4FY43_LEIMA	Q4fy43	leishmania
23	30	90.9	615	2	Q68EG6_BRARE	Q68eg6	brachydanio
24	30	90.9	693	2	Q4WWH0_ASPFU	Q4wwh0	aspergillus
25	30	90.9	699	2	Q5LA02_BACFN	Q5la02	bacteroides
26	30	90.9	699	2	Q64QB0_BACFR	Q64qb0	bacteroides
27	30	90.9	1196	2	Q55L50_CRYNE	Q55l50	cryptococcu
28	30	90.9	1196	2	Q5KAD1_CRYNE	Q5kad1	cryptococcu
29	30	90.9	1379	2	Q4Y3V7_PLACH	Q4y3v7	plasmodium
30	30	90.9	4844	2	Q5KAK5_CRYNE	Q5kak5	cryptococcu
31	30	90.9	4852	2	Q55KX4_CRYNE	Q55kx4	cryptococcu
32	29	87.9	113	2	Q6A1P1_EUPVA	Q6alp1	euplotes va
33	29	87.9	184	2	Q6NGB8_CORDI	Q6ngb8	corynebacte
34	29	87.9	196	2	Q6ZIW2_ORYSA	Q6ziw2	oryza sativ
35	29	87.9	210	2	Q5QLN8_ORYSA	Q5qln8	oryza sativ
36	29	87.9	250	2	O17154_CAEEL	O17154	caenorhabdi
37	29	87.9	260	2	Q9DEC9_CHICK	Q9dec9	gallus gall
38	29	87.9	267	2	Q2KZ01_BORAV	Q2kz01	bordetella
39	29	87.9	285	2	Q5FIL5_LACAC	Q5fil5	lactobacill
40	29	87.9	365	2	Q5AEZ1_CANAL	Q5aez1	candida alb
41	29	87.9	402	2	Q5BEB2_EMENI	Q5beb2	aspergillus
42	29	87.9	421	2	Q56VX9_CAEEL	Q56vx9	caenorhabdi
43	29	87.9	433	2	Q3P1Z3_9GAMM	Q3p1z3	shewanella
44	29	87.9	468	1	YSO1_CAEEL	Q10127	caenorhabdi
45	29	87.9	486	2	Q8WQA7_CAEEL	Q8wqa7	caenorhabdi
46	29	87.9	486	2	Q96796_FLV	Q96796	feline leuk
47	29	87.9	495	2	Q4XT57_PLACH	Q4xt57	plasmodium
48	29	87.9	497	2	Q96793_FLV	Q96793	feline leuk
49	29	87.9	497	2	Q96794_FLV	Q96794	feline leuk
50	29	87.9	513	2	Q4YQA8_PLABE	Q4yqa8	plasmodium
51	29	87.9	540	2	Q4S4Q7_TETNG	Q4s4q7	tetraodon n
52	29	87.9	547	2	Q96795_FLV	Q96795	feline leuk
53	29	87.9	554	2	Q2ZE60_CALSA	Q2ze60	caldicellul
54	29	87.9	586	2	Q5AEK7_CANAL	Q5aek7	candida alb
55	29	87.9	590	2	Q4TC98_TETNG	Q4tc98	tetraodon n
56	29	87.9	640	2	Q2UCC0_ASPOR	Q2ucc0	aspergillus
57	29	87.9	641	2	Q98UI4_CHICK	Q98ui4	gallus gall
58	29	87.9	652	2	Q7RM64_PLAYO	Q7rm64	plasmodium
59	29	87.9	773	2	Q96JU8_HUMAN	Q96ju8	homo sapien
60	29	87.9	781	2	Q65JG3_BACLD	Q65jg3	bacillus li
61	29	87.9	857	2	Q4Q6R8_LEIMA	Q4q6r8	leishmania
62	29	87.9	892	2	Q9U299_CAEEL	Q9u299	caenorhabdi
63	29	87.9	957	2	Q5CS61_CRYPV	Q5cs61	cryptospori
64	29	87.9	1154	2	Q3U1W7_MOUSE	Q3ulw7	m b6-derive
65	29	87.9	2471	1	NOTC2_HUMAN	Q04721	homo sapien